

บทบาทของแองจิโอเทนซินต่อการแสดงออกของยีนและโปรตีนไตไฮโดรโฟเลต

รีดักเทส จีทีพีไซโคลไฮโดรเลส 1 และไนตริกออกไซด์ซินเทสในไต

ในภาวะที่ไตขาดเลือดไปเลี้ยงชั่วคราว



นางสาวอยู่เย็น ชื้อจ่าง

สถาบันวิทยบริการ
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ลิขสิทธิ์ของจุฬาลงกรณ์มหาวิทยาลัย

ROLE OF ANGIOTENSIN IN RENAL DIHYDROFOLATE
REDUCTASE, GTP-CYCLOHYDROLASE 1 AND NITRIC OXIDE
SYNTHASE EXPRESSION IN RENAL ISCHEMIC REPERFUSION



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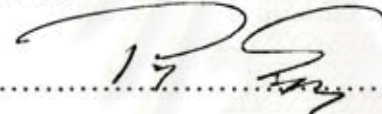
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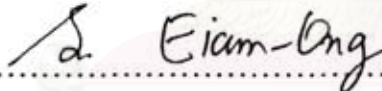
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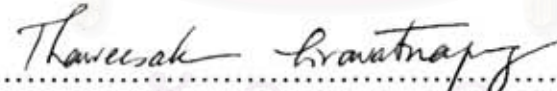
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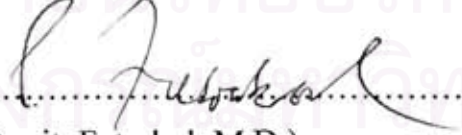

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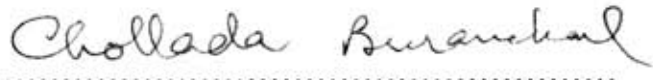
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อยู่เย็น ชื่อจ้าง: บทบาทของแองจิโอเทนซิน ต่อการแสดงออกของยีนและโปรตีน ไคไฮโดรโฟเลตรีดักเทส จีทีพีไซโคลไฮโดรเลส 1 และไนตริกออกไซด์ซินเทสในไต ในภาวะที่ไตขาดเลือดไปเลี้ยงชั่วคราว (Role of angiotensin in renal dihydrofolate reductase, GTP-cyclohydrolase 1 and nitric oxide synthase expression in renal ischemic reperfusion) อ. ที่ปรึกษา : รศ. ดร. สมจิตร เยี่ยมอ่อน, อ. ที่ปรึกษาร่วม : อ. ดร. ทวีศักดิ์ ตีระวัฒนพงษ์, 91 หน้า.

ภาวะที่ไตขาดเลือดไปเลี้ยงชั่วคราวเพิ่มระดับแองจิโอเทนซิน 2 (ANG II) การศึกษาจากการเพาะเลี้ยงเซลล์ พบว่า แองจิโอเทนซิน 2 ลดระดับไคไฮโดรโฟเลตรีดักเทส (DHFR) แต่ไม่เปลี่ยนแปลงระดับจีทีพีไซโคลไฮโดรเลส 1 (GTP-CH 1) พบว่าเอนไซม์ทั้งสองตัวนี้ถูกใช้เพื่อสร้างบีเอช 4 (BH4) ซึ่งมีบทบาทสำคัญต่อการเป็นโครงสร้างคู่ (dimer) ของไนตริกออกไซด์ซินเทส (NOS) แต่ยังไม่มีการศึกษาบทบาทของ แองจิโอเทนซิน 2 ต่อการแสดงออกพร้อมๆ กันของยีนและโปรตีนของไคไฮโดรโฟเลตรีดักเทส จีทีพีไซโคลไฮโดรเลส 1 และไนตริกออกไซด์ซินเทส ในภาวะที่ไตขาดเลือดไปเลี้ยงชั่วคราว การวิจัยครั้งนี้ทำการทดลองในหนูแรทพันธุ์ดำซึ่งแบ่งออกเป็น 2 กลุ่มใหญ่ๆ คือ กลุ่ม sham (S) และกลุ่มที่ชักนำให้เกิดภาวะขาดเลือดไปเลี้ยงชั่วคราวที่ไตข้างซ้าย โดยการอุดกั้นหลอดเลือดเลี้ยงไตเป็นเวลา 30 นาที และให้เลือดไปเลี้ยงไตดังเดิมเป็นเวลา 1 วัน (IR) ซึ่งทั้ง 2 กลุ่มนี้จะถูกแบ่งเป็นอีก 3 กลุ่มย่อย คือ 1) ได้รับน้ำดื่มเพียงอย่างเดียว หรือ 2) ได้รับน้ำดื่มผสม angiotensin converting enzyme inhibitor (ACEI; Enalapril[®]; 5 mg/kg/day) หรือ 3) ได้รับน้ำดื่มผสม angiotensin II receptor type 1 blocker (ARB; Losartan[®]; 10 mg/kg/day) สัตว์ทดลองจะได้รับการดักถ่าย 1 วันก่อนการผ่าตัดทำ S หรือ IR และรับต่อไปอีกเป็นเวลา 1 วันหลังการผ่าตัด เมื่อครบกำหนดการทดลองทำการเก็บตัวอย่างปัสสาวะและเลือดเพื่อตรวจวัดระดับอิเล็กโทรไลต์ สารยูเรียไนโตรเจน ครีเอตินีน และคำนวณค่าครีเอตินีนเคลียแรนซ์ รวมทั้งเก็บตัวอย่างเนื้อไต เพื่อแยก RNA และตรวจวัดระดับการแสดงออกของยีน (mRNA) และโปรตีนของไคไฮโดรโฟเลตรีดักเทส จีทีพีไซโคลไฮโดรเลส 1 เอนโดซีเลียมและอินดิวิจิบิลไนตริกออกไซด์ซินเทส โดยวิธี Reverse transcriptase polymerase chain reaction (RT-PCR) และ Western blot ตามลำดับ ผลการทดลองพบว่า IR ลดระดับไคไฮโดรโฟเลตรีดักเทส ทั้งการแสดงออกของยีนและโปรตีน ($p < 0.01$) ซึ่งมีค่าเพิ่มขึ้นเมื่อให้ ACEI ($p < 0.05$) หรือ ARB ($p < 0.01$) ในขณะที่ระดับจีทีพีไซโคลไฮโดรเลส 1 มีค่าเท่าเดิม IR ลดระดับเอนโดซีเลียมไนตริกออกไซด์ซินเทสโครงสร้างคู่ ($p < 0.01$) แต่เพิ่มระดับเอนโดซีเลียมไนตริกออกไซด์ซินเทสโครงสร้างเดี่ยว (monomer) ($p < 0.01$) ซึ่งระดับดังกล่าวมีค่ากลับคืนเมื่อให้ ACEI หรือ ARB ($p < 0.01$) ระดับการแสดงออกของยีนและโปรตีนรวมของเอนโดซีเลียมไนตริกออกไซด์ซินเทส (total eNOS protein) มีค่าไม่เปลี่ยนแปลงในทุกกลุ่มการทดลอง แต่ IR เพิ่มระดับการแสดงออกของยีน โปรตีนรวม และโครงสร้างเดี่ยวของอินดิวิจิบิลไนตริกออกไซด์ซินเทส ($p < 0.01$) ซึ่งมีระดับลดลงโดย ACEI หรือ ARB ($p < 0.01$)

การศึกษานี้แสดงให้เห็นครั้งแรกที่บ่งว่า ภาวะที่ไตขาดเลือดไปเลี้ยงชั่วคราว โดยมีการกระตุ้นผ่านแองจิโอเทนซิน 2 นั้น ลดระดับไคไฮโดรโฟเลตรีดักเทส แต่เพิ่มอินดิวิจิบิลไนตริกออกไซด์ซินเทส ทั้งการแสดงออกของยีนและโปรตีน ภาวะ IR เพิ่มระดับโครงสร้างเดี่ยว แต่ลดระดับโครงสร้างคู่ของเอนโดซีเลียมไนตริกออกไซด์ซินเทส การยับยั้งแองจิโอเทนซิน 2 ด้วย ACEI หรือ ARB สามารถเพิ่มระดับไคไฮโดรโฟเลตรีดักเทสและเอนโดซีเลียมไนตริกออกไซด์ซินเทสโครงสร้างคู่ ซึ่งในขณะเดียวกันสามารถลดระดับอินดิวิจิบิลไนตริกออกไซด์ซินเทสและไนตริกออกไซด์ซินเทสโครงสร้างเดี่ยวที่เพิ่มสูงขึ้น พบว่า IR ไม่มีผลต่อจีทีพีไซโคลไฮโดรเลส 1 การศึกษานี้ยังบ่งชี้อีกด้วยว่า ANG II receptor type 1 แสดงบทบาทสำคัญในการควบคุมการแสดงออกของ ไคไฮโดรโฟเลตรีดักเทส และไนตริกออกไซด์ซินเทส

ภาควิชา สรีรวิทยา

สาขาวิชา สหสาขาวิชาสรีรวิทยา

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ลายมือชื่อนิสิต..... *อยู่เย็น ชื่อจ้าง*

ลายมือชื่ออาจารย์ที่ปรึกษา..... *S. J. Escobar*

ลายมือชื่ออาจารย์ที่ปรึกษาร่วม..... *ทวีศักดิ์ ตีระวัฒนพงษ์*

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KEY WORD: ANGIOTENSIN/ DIHYDROFOLATE REDUCTASE/ GTP-CYCLOHYDROLASE 1/ NITRIC OXIDE SYNTHASE/ RENAL ISCHEMIC REPERFUSION

YUYEN SEUJANGE: ROLE OF ANGIOTENSIN IN RENAL DIHYDROFOLATE REDUCTASE, GTP-CYCLOHYDROLASE 1 AND NITRIC OXIDE SYNTHASE EXPRESSION IN RENAL ISCHEMIC REPERFUSION. THESIS ADVISOR: ASSOC. PROF. SOMCHIT EIAM-ONG, Ph.D., THESIS CO-ADVISOR: THAWEESEK TIRAWATNAPONG, Ph.D., 91 pp.

Renal ischemic reperfusion (IR) enhances angiotensin II (ANG II) level. In cell culture study, ANG II suppresses dihydrofolate reductase (DHFR) but not modulate GTP-cyclohydrolase I (GTP-CH 1) expression. Both enzymes are required for synthesis of BH₄ which plays a crucial role in dimerization of nitric oxide synthase (NOS). There is no simultaneous study the role of ANG II on renal DHFR, GTP-CH 1, NOS gene and protein expression during IR. Male Wistar rats were divided into two main groups: sham (S) or IR (30-minute renal pedicle occlusion and reperfusion for 1 day). Both groups were further treated with 1) water, or 2) angiotensin converting enzyme inhibitor (ACEI; Enalapril®; 5 mg/kg/day), or 3) angiotensin II receptor type I blocker (ARB; Losartan®; 10 mg/kg/day) for one day before S or IR and continuously for 1 day after the operation. On each experimental due date, 24-hr urine and blood samples were collected. The serum was determined for electrolytes, blood urea nitrogen, creatinine (Cr), and Cr clearance (CCr). The kidneys were removed for RNA isolation, detection of mRNA expression (RT-PCR), and protein abundance (Western blot) for DHFR, GTP-CH 1, endothelial NOS (eNOS), and inducible NOS (iNOS). The data show that IR decreased DHFR mRNA and protein levels ($p < 0.01$) which were restored by ACEI ($p < 0.05$) or ARB ($p < 0.01$); whereas GTP-CH 1 expression was remained. IR suppressed the eNOS dimer ($p < 0.01$) while enhanced the monomer ($p < 0.01$) which were corrected by ACEI or ARB ($p < 0.01$). The renal eNOS mRNA and total eNOS protein levels did not change in all experimental groups. IR increased iNOS mRNA, total iNOS protein, and iNOS monomer ($p < 0.01$) which were reduced by ACEI or ARB ($p < 0.01$).

The present study demonstrates the first evidence indicating that IR, via stimulation of ANG II, suppresses renal DHFR but activates iNOS both mRNA and protein expression. IR enhances the monomer while diminishes the dimer form of eNOS. Inhibition of ANG II by using ACEI or ARB could restore DHFR and eNOS dimer whereas attenuate the heightened levels of iNOS expression and NOS monomer. IR has no effect on GTP-CH 1 expression. The present result also indicates that angiotensin II receptor type I plays a crucial role in modulation of DHFR and NOS expression.

Field of study Physiology

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LIST OF ABBREVIATIONS

ACE	Angiotensin converting enzyme
ACEI	Angiotensin converting enzyme inhibitor
ANG II	Angiotensin II
ARB	Angiotensin II receptor type 1 blocker
ARF	Acute renal failure
AT1	Angiotensin II receptor type 1
AT2	Angiotensin II receptor type 2
BH4	5,6,7,8-Tetrahydrobiopterin
BH2	7,8-dihydrobiopterin
BUN	Blood urea nitrogen
Cr	Creatinine
CCr	Creatinine clearance
cDNA	Complementary deoxyribonucleic acid
°C	Degree Celsius
DHFR	Dihydrofolate reductase
DNA	Deoxyribonucleic acid
dNTP	Deoxynucleotide triphosphates
eNOS	Endothelial nitric oxide synthase
GAPDH	Glyceroldehyde-3-phosphate-dehydrogenase
GFR	Glomerular filtration rate
FAD	Flavin adenine dinucleotide
FMN	Flavin mononucleotide
GTP-CH 1	GTP-Cyclohydrolase 1
H ₂ O ₂	Hydrogen peroxide

iNOS	Inducible nitric oxide synthase
IFN- γ	Interferon- γ
IR	Ischemic reperfusion
LPS	Lipopolysaccharide
LT-PAGE	Low temperature sodium dodecyl sulfate-polyacrylamide gel electrophoresis
MAP	Mean arterial pressure
M	Molar
M-MLV	Malony murine leukemia virus
mRNA	Messenger ribonucleic acid
NADPH	nicotinamide adenine dinucleotide phosphate (oxidized form)
NO	Nitric oxide
NOS	Nitric oxide synthase
nNOS	neuronal nitric oxide synthase
ONOO \cdot	Peroxynitrite
O $_2$ \cdot	Superoxide
RBF	Renal blood flow
RT-PCR	Reverse transcriptase polymerase chain reaction
SDS-PAGE	Sodium dodecyl sulfate-polyacrylamide gel electrophoresis
VR	Vascular resistance
μ l	Microlitre

CHAPTER I

INTRODUCTION

BACKGROUND AND RATIONALE

Renal ischemic reperfusion (IR) is characterized by a decline in renal blood flow (RBF) and oxygen supply (Waz et al., 1998). This often occurs during renal transplantation, surgical revascularization of the renal artery, resuscitation from hypotension states, and treatment of suprarenal aortic aneurysms (Rhoden et al., 2001).

In renal IR, a reduction in blood pressure causes renin release (Allred et al., 2000; Bivol et al., 2005), and also increases angiotensin converting enzyme (ACE) activity (Guan et al., 1992), then enhances angiotensin II (ANG II) levels (Allred et al., 2000; Kontogiannis and Burns, 1998). In addition to its hemodynamic effects directly, ANG II could affect nitric oxide (NO) production, NO synthase (NOS) expression and function via alteration of tetrahydrobiopterin (BH₄) synthesis (Chalupsky and Cai, 2005; Hennington et al., 1998). BH₄ is one of essential co-factors for dimerization of NOS to be an active form (Kakoki et al., 2000). Deficiency of BH₄ causes NOS uncoupling which produces superoxide (O₂^{•-}) instead of NO (Chalupsky and Cai, 2005; Kakoki et al., 2000).

Generally, BH₄ could be produced by de novo or salvage pathway (Thony et al., 2000). The former uses GTP-cyclohydrolase 1 (GTP-CH 1) whereas the latter requires dihydrofolate reductase (DHFR) (Thony et al., 2000). Recently, Chalupsky and Cai (2005) have demonstrated that ANG II rapidly and transiently activates NADPH oxidase to produce O₂^{•-}, leading to hydrogen peroxide (H₂O₂)-dependent

down-regulation of DHFR in bovine aortic endothelial cell culture (BAEC). In addition, a second phase of O_2^{\cdot} production from uncoupled NOS has also been noted (Chalupsky and Cai 2005). The overexpression of DHFR could restore NO production and abolish O_2^{\cdot} production from uncoupled NOS in ANG II stimulated cells (Chalupsky and Cai, 2005). These data characterize an essential role of DHFR in maintaining BH4 and NO bioavailability, and ANG II also modulates DHFR under this circumstance. However, the exogenous H_2O_2 could up-regulate GTP-CH 1 expression which increases total biopterin, but the endogenous H_2O_2 produced by ANG II does not modulate GTP-CH 1 (Chalupsky and Cai, 2005; Shimizu et al., 2003). These results indicate that DHFR is much more sensitive to lower endogenous H_2O_2 compared to GTP-CH 1, which is regulated only in response to exogenous H_2O_2 .

As noted above, during renal IR a rise in ANG II occurs. This would modulate the expression of either DHFR or GTP-CH 1, or both and subsequently influence on NOS expression. However, there is no study on IR in the relation to renal DHFR, GTP-CH 1, and NOS expression simultaneously as well as the role of ANG II and ANG II receptor type 1 in this circumstance. Therefore, the present study aims to investigate this regard.

RESEARCH QUESTIONS

1. Does IR have any effects on renal DHFR, GTP-CH 1, eNOS and iNOS expression?
2. Does angiotensin inhibition has an influence on renal DHFR, GTP-CH 1, eNOS and iNOS expression in IR? If so, is it mediated via angiotensin receptor type 1?

RESEARCH OBJECTIVES

1. To study the changes of renal DHFR, GTP-CH 1, eNOS and iNOS expression in IR.
2. To study the role of angiotensin in renal DHFR, GTP-CH 1, eNOS and iNOS expression in IR.
3. To study the role of angiotensin receptor type 1 in the changes of renal DHFR, GTP-CH 1, eNOS and iNOS expression in IR.

HYPOTHESIS

1. IR would decrease renal DHFR and eNOS expression but increase GTP-CH 1 and iNOS.
2. Angiotensin inhibition could restore those changes of renal DHFR, GTP-CH 1, eNOS and iNOS expression in IR.
3. Angiotensin receptor type 1 involves in the changes of renal DHFR, GTP-CH 1 eNOS and iNOS expression in IR.

KEY WORDS

angiotensin

dihydrofolate reductase

GTP-cyclohydrolase 1

nitric oxide synthase

renal ischemic reperfusion

EXPECTED BENEFIT AND APPLICATION

The results would provide further supporting data for the role of angiotensin on DHFR, GTP-CH 1, eNOS, and iNOS expression in renal IR model.



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CHAPTER II

THEORY AND LITERATURE REVIEW

RENAL ISCHEMIC REPERFUSION

Renal ischemic reperfusion (IR) occurs in clinical practice and is a consequence of systemic hypoperfusion with subsequent circulatory resuscitation (Jefayri et al., 2000). Local renal hypoperfusion after aortic cross clamping or renal transplantation also causes IR injury to the kidney (Jefayri et al., 2000). Renal IR is an important cause of renal dysfunction often leading to acute renal failure (ARF), causing high mortality among patients in intensive care who require dialysis (Deng et al., 2001). The severity of the injury depends on the duration of ischemia and subsequent reperfusion (Aragno et al., 2003). Reperfusion, although essential for the survival of ischemic renal tissue, causes additional damage (Aragno et al., 2003).

A decrease in RBF is of critical importance in initiating and extending the pathophysiology of ischemic ARF (Molitoris and Sutton, 2004). Under physiologic conditions, the oxygen tension of the kidney decreases as one moves from the outer cortex to the inner medulla (Brezis and Rosen, 1995). Regional alterations in RBF persist after the ischemic event and play an important role in the extension phase or renal ischemic injury. During reperfusion a reduction in total RBF of 40% to 50% of normal has been reported in both animal models of ischemic ARF and in human ischemic ARF (Lieberthal, 1997). Studies have demonstrated a persistent reduction in RBF contributes significantly to the diminished glomerular filtration rate (GFR) observed in human allografts following ischemic ARF (Alejandro et al., 1995). Mechanisms involved in the alteration of renal perfusion following ischemic injury

are incompletely understood. An imbalance between mediators of renal vasoconstriction and renal vasodilatation has been proposed to play a role in animal models of ischemic ARF. The two molecules that have been widely studied and very implicated in renal IR injury are ANG II and NO.

ANGIOTENSIN II

ANG II is a potent vasoconstrictor that produced by renin angiotensin cascade (Levens et al., 1992). The enzyme renin is secreted by the kidney into the blood in response to a number of stimuli, including a reduction in blood pressure and a reduction in extracellular fluid volume. Renin cleaves 10 amino acids from its α -globulin substrate angiotensinogen to form the decapeptide ANG I. ANG I is rapidly converted to the biologically active octapeptide (ANG II) upon circulation through organs, by the action of the endothelial enzyme ANG converting enzyme (ACE) (Levens et al., 1992).

Generation of ANG II acts to constrict vascular smooth muscle cells and also modulates aldosterone secretion, catecholamine release and secretion of pituitary peptides and hormones (Wong et al., 1990). Within the kidney, ANG II modulates GFR by exerting direct effects on afferent and efferent arteriolar tone and on mesangial cell function (Ichikawi and Harris, 1991). The proximal tubule (PT) contains mRNA for all components of the renin angiotensin system. High levels of ANG II are present in proximal tubular lumen, this suggests that ANG II is synthesized locally and can act in an autocrine or paracrine fashion on tubular cells (Kontogiannis and Burns, 1998). ANG II mediates its effect in the renal vasculature through two main G-coupled receptors, the AT1 and AT2 receptors (Bivol et al., 2005; Murphy et al., 1991). The rat has two types of AT1 receptors, the AT1_A and

AT1_B receptors, which have 95% homology in their receptor amino acid sequences (Kakar et al., 1992). However, in the human kidney, only a single gene encoding for the AT1 receptor is expressed (Curnow et al., 1992). AT1 receptor distribution is widespread in the kidney such as in the vasculature on both smooth muscle plasma membranes and endothelial cells including afferent and efferent arterioles (Ardailou, 1999) as well as in the PT (Gunning et al., 1996). The AT2 receptor has only 34% homology with the AT1 receptor and is expressed at the low level, particularly in the renal vasculature (Douglas and Hopfer, 1997). Moreover, the localization and function of AT2 receptor in the adult kidney remain unclear (Kontogiannis and Burns, 1998).

In IR condition, a reduction in blood pressure causes renin release (Allred et al., 2000; Bivol et al., 2005), and also increases ACE activity (Gaun et al., 1992), subsequently enhances ANG II levels (Allred et al., 2000; Kontogiannis et al., 1998). The role of ANG II during IR is extraordinary complex. Generation of ANG II acts to raise perfusion pressure and to protect glomerular filtration by efferent arteriolar constriction (Lerman and Textor, 2001). Because the efferent arteriole constricts at lower ANG II concentrations (10^{-11} M) than the afferent arteriole (10^{-9} M) (Ito et al., 1993). This will primarily constrict the efferent arteriole but possibly also the afferent arteriole if ANG II increases sufficiently (Sorensen et al., 2004). The rat model with IR shows renal damage, increased vascular resistance (VR) and mean arterial pressure (MAP) as well as decreased RBF (Sadjadi et al., 2002; Vargas et al., 1994). ACE inhibitor (ACEI) (Vargas et al., 1994) or AT1 receptor blocker (ARB) (Barrilli et al., 2004; Kontogiannis and Burns, 1998) could ameliorate renal damage, decrease VR and MAP and also increase RBF (Bivol et al., 2005; Vargas et al., 1994). The results suggest that ANG II acting via the AT1 receptor plays a role in the

development of renal damage after IR. In addition to its hemodynamic effects directly, the recent study have demonstrated that ANG II could affect NO production, NOS expression and function via alteration of BH₄ synthesis (Chalupsky and Cai, 2005; Hennington et al., 1998).

NITRIC OXIDE AND NITRIC OXIDE SYNTHASES

NO is a free radical gas that could diverse biomessenger function and participate in the regulation of kidney function by counteracting the vasoconstrictor effects of ANG II (Lerman and Textor, 2001). NO is a potent activator of guanylate cyclase, an important hemo-protein target of NO (Lane and Gross., 1999). Binding of NO alters the conformation of the heme moiety and causes activation of the enzyme. The subsequent rise in cGMP levels causes the activation of cGMP-dependent kinases and also augment Ca²⁺-extrusion through the plasma membrane Ca²⁺-ATPase (Masden et al., 2000). These result in vascular smooth muscle cells relaxation, suppression of platelet adhesion and aggregation (Azuma et al., 1986; Masden et al., 2000).

NO is synthesized from L-arginine by a family of NOS (Schwobel et al., 2000). There are three distinct isoforms of the enzyme (Marsden et al., 2000), nNOS (Bredt and Snyder, 1990; Mayer et al., 1990), eNOS (Lamas et al., 1992; Pollock et al., 1991), which partake in signalling cascades, are constitutively expressed and depend on the presence of Ca²⁺ for activity (Lane and Gross, 1999). However, the recent study has demonstrated that cNOS activity could be activated via either Ca²⁺-dependent or Ca²⁺-independent pathway (Cai et al., 2003). For example, H₂O₂ causes an acute and potent NO release from endothelial cells that is mediated by additive effects of the phosphatidylinositol 3-kinase/Akt-dependent eNOS serine 1179

phosphorylation and MEK/ERK $\frac{1}{2}$ activation (Cai et al., 2003). In the kidney, the expression of nNOS is limited mainly to the macula densa and its regulatory role in signal transduction within the juxtaglomerular apparatus (Mundel et al., 1992). The eNOS is constitutively expressed by the endothelial lining in blood vessels of different caliber (Roczniak et al., 2000; Kone, 1997). The iNOS isoform is involved in the nonspecific immune response, regulated transcriptionally, and only expressed in response to cytokines, once expressed, it remains active in the absence of Ca^{2+} and will sustain continuous NO synthesis for days (Hevel et al., 1991; Stuehr et al., 1991; Lane and Gross, 1999). Surprisingly, iNOS is also expressed constitutively in several segments of the renal tubule as well as in the glomerulus, interlobar and arcuate arteries of the normal rat kidney (Mattson et al., 2000).

ANGIOTENSIN II AND NITRIC OXIDE SYNTHASES

The effects of ANG II on regulation of NOS and NO were extensively performed both in vitro and in vivo studies. Incubation of ANG II in various cell cultures alters NO production, NOS activity, and NOS expression. For example, in cultured bovine pulmonary artery endothelial cell (BPAE), eNOS mRNA was significantly increased 2.4-fold 6 h after the additional of ANG II (10^{-6} M) over basal levels. In a similar time course, it was found that eNOS protein concentrations are increased 247% over basal levels at 4 h after ANG II addition. There is a second protein peak at 8 h after ANG II treatment in which eNOS was increased 333% over basal (Olson et al., 1997). These data suggest that ANG II stimulate eNOS mRNA expression and are followed by increased levels of eNOS protein in cultured BPAE cells, consistent with an observed increase in nitrite (NO metabolite) production (Olson et al., 1997). Both the increase in eNOS protein and mRNA expression could

be attenuated with the ARB (saralasin) (Olson et al., 1997). Moreover, Olson et al. (2004) further demonstrated that ANG II could activate eNOS protein expression as a dose- and time-dependent, as well as activate eNOS mRNA expression and NO production in cultured BPAE cells. However, PD-123319, an AT₂ receptor blocker could attenuate the heightened levels (Olson et al., 2004). These data indicate that ANG II activated eNOS expression and NO generation via both AT₁ and AT₂ receptor. These stimulatory effects have also been observed in coronary microvascular endothelial cell (Bayraktutan and Ulker, 2003) and in ovine fetoplacental artery endothelium (Zheng et al., 2005).

Regarding to in vivo studies, an infusion of ANG II increased eNOS protein expression in myocardium via AT₁ receptor (Tambascia et al., 2001). On the contrary, the eNOS mRNA and protein levels as well as NOS activity in the left ventricular are markedly decreased in the rat that given ANG II (200 ng/kg/min) for two weeks. The levels are significantly ameliorated by ARB, TCV-116 (Kobayashi et al., 2001). In the kidney, more intricate data have been noted. ANG II administration in rat increases NO production, NOS activity, and NOS expression (Chin et al., 1999; Zou et al., 1998). However, these alterations are variable and seem to depend on the period of ANG II exposure. For example, an acute ANG II infusion (110 minutes) increases eNOS mRNA in kidney by 70% without changing eNOS protein levels, whereas a chronic infusion (10 days) enhances eNOS protein by 90% without changing eNOS mRNA levels (Hennington et al., 1998). Moreover, Moreno et al. (2002) have also shown that ANG II infusion for 3 h increases renal cNOS activity without modification of their protein expression while a chronic ANG II (3 d) could augment the protein expression but not the activity. Furthermore, action of ANG II in the kidney is likely to be area specific regulation on NOS expression. For instance,

ANG II administration could up-regulate eNOS mRNA and protein in renal cortex, but not in renal medulla (Chin et al., 1999; Navar et al., 2000).

Moreover, the recent study has also demonstrated the effect of ANG II on iNOS expression. For example, in the transgenic rats that over expressed both human renin and angiotensinogen genes (dTGR) feature ANG II-induced iNOS protein expression (Theuer et al. 2005). In addition, an infusion of ANG II enhances iNOS mRNA level in aortic artery by activating of NF- κ B cascade (Tham et al., 2002). Blocking ANG II by using losartan, an AT1 receptor blocker, can have protective effects on the renal injury in glomerulosclerosis by down-regulating the expressions of iNOS (Ji et al., 2005). The data indicate that ANG II could modify eNOS and iNOS at either a transcriptional or translational level.

Besides the effects on NOS expression and NO production, ANG II could increase O_2^{\cdot} generation through activating membrane associated NADH/NADPH oxidase activity (Berry et al., 2000; Ushio-Fukai et al., 1996). The excessive O_2^{\cdot} can interact with NO, which reduces NO bioavailability to generate peroxynitrite ($ONOO^{\cdot}$), a potent oxidative stress (Walker et al., 2000). Moreover, the negative charged O_2^{\cdot} radical is unstable in aqueous solution (half-life of a few seconds) and is rapidly dismutated to H_2O_2 (Li et al., 2004). Interestingly, the recent study in BAEC has demonstrated that H_2O_2 produced by ANG II could affect NOS function via changing in BH4 synthesis (Chalupsky and Cai, 2005). BH4 is one of essential co-factors for dimerization of NOS to be an active form (Kakoki et al., 2000; Thony et al. 2000). Deficiency of BH4 causes NOS uncoupling which produces O_2^{\cdot} instead of NO (Chalupsky et al., 2005; Kakoki et al., 2000).

TETRAHYDROBIOPTERIN AND NITRIC OXIDE SYNTHASES

BH₄, an essential co-factor for various processes, and is present in probably every cell or tissue of higher organisms (Thony et al., 2000). BH₄ is required for various enzyme activities, and for less defined functions at the cellular level (Thony et al., 2000). One of the most investigated functions of BH₄ is its action as a co-factor of NOS (Thony et al., 2000).

As mentioned earlier, all three NOS isoforms are the enzymes that catalyzes the production of NO and L-citrulline from L-arginine, O₂, and NADPH-derived electrons (Channon, 2004; Mayer and Hemmens, 1997). NOS utilizes six different co-factors and prosthetic groups: thiolate-bound heme (Klatt et al., 1992; Stuehr and Ikeda-Saito, 1992), FAD and FMN (Hevel et al., 1991; Stuehr et al., 1991), calmodulin/Ca²⁺ (Cho et al., 1992; Mayer et al., 1989), BH₄ (Mayer et al., 1990; Pollock et al., 1991), and Zn²⁺ (Hemmens et al., 2000; Miller et al., 1999) (Figure A)

The enzyme functions as a dimer consisting of two identical monomer (Figure B, left side), which can be functionally and structurally divided into two major domain, a C-terminal reductase domain and N-terminal oxygenase domain (Figure A and B) (Channon, 2004; Hemmens and Mayer, 1998). The former contains binding sites for one molecule each of NADPH, FAD, and FMN, whereas the latter binds heme and BH₄, as well as the substrate L-arginine (Andrew and Mayer, 1999). Between these two regions lies the calmodulin (CaM) binding domain, which plays a key role in both the structure and function (Figure A) (Andrew and Mayer, 1999).

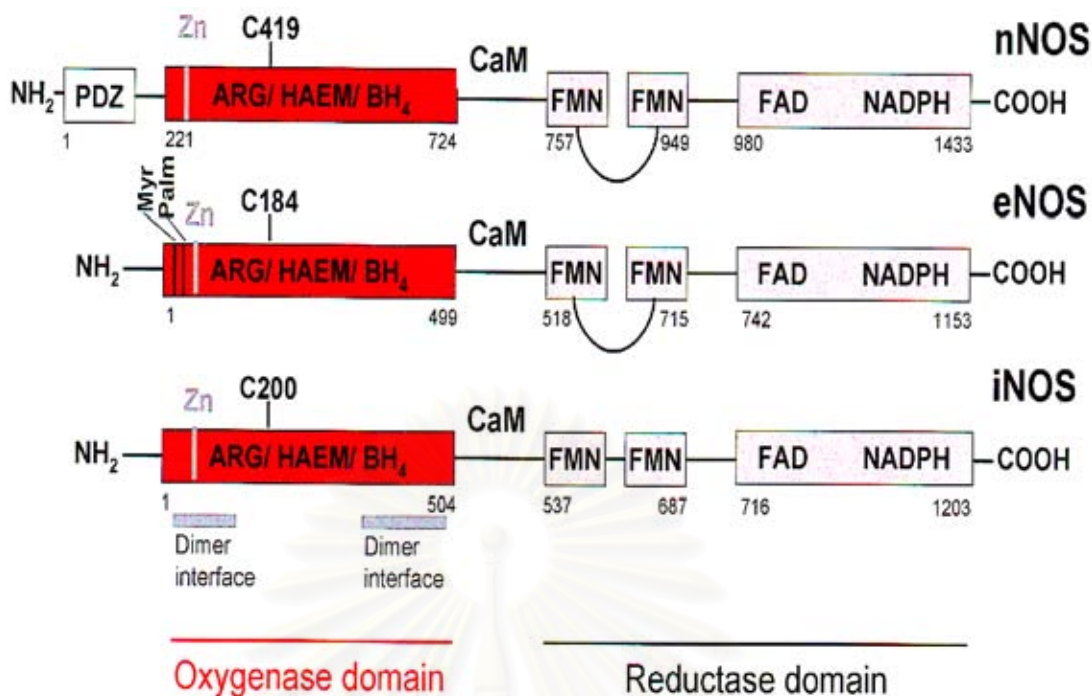


Figure A: The domain structure of human nNOS, eNOS and iNOS. Oxygenase, reductase and PDZ domains are denoted by solid boxes and the amino acid residue number at the start/end of each domain is shown. The cysteine residue which ligates the haem and the CaM-binding site is indicated for each isoform, myristoylation (Myr) and palmitoylation (Palm) sites on eNOS are shown, as is the location of the zinc-ligating cysteines (Zn in grey). The autoinhibitory loop within the FMN regions of nNOS and eNOS are also shown and grey bars indicate the dimer interface in the oxygenase domain.

NOS catalyzes the formation of NO in two consecutive steps, as shown in Figure B (right side) (Stuehr et al., 1991). First, L-arginine is oxidized to *N*^G-hydroxy-L-arginine (NHA), in a reaction that consumes one molecule of O₂ and two NADPH-derived electrons. Subsequently, NHA is converted into L-citrulline and NO with consumption of one more NADPH-derived electron and another molecule of O₂. This affords an overall stoichiometry of 1.5 NADPH oxidized per NO produced (Gorren et al., 2000; Griffith and Stuehr, 1995).

The catalytic center of NOS is a heme that is located in the oxygenase domain and heme has a cysteinyl thiolate for an axial ligand (Ghosh and Stuehr, 1995; Sheta et al., 1994). The substrate arginine binds close to the heme but without direct interaction (Fischmann et al., 1999; Raman et al., 1998). The function of the flavins is the same as in cytochrome P450 reductase. Electrons are transferred from NADPH via FAD and FMN to the heme in the oxygenase domain. FAD accepts two electrons at a time, but transfers them one by one to the FMN semiquinone, with reduced FMN functioning as a one electron donor to the heme (Noble et al., 1999). Calmodulin conveys a conformational change that is necessary for interdomain electron transfer (Abu-Soud and Stuehr, 1993; Sheta et al., 1994), and that also facilitates intradomain electron transfer, *i.e.* from FAD to FMN (Abu-Soud et al., 1994). This renders the constitutive isoforms sensitive to Ca^{2+} (Lamas et al., 1992; Mayer et al., 1990), in accordance with their role in cell signalling. The much higher affinity for calmodulin of iNOS enables this isoform to remain active in the absence of Ca^{2+} (Cho et al., 1992). The latest addition to the list of cofactors, Zn^{2+} , binds to NOS in a stoichiometry of 1 per dimer, where it is coordinated to four cysteinyl sulfur atoms (2 from each monomer) in the dimer interface (Fischmann et al., 1999; Li et al., 1999). It plays an important role in dimer stabilization, but is not essential for catalysis (Hemmens et al., 2000; Miller et al., 1999). BH4 binds to the oxygenase domain in the immediate vicinity of the heme and the substrate arginine, though not in the distal heme pocket. Instead it is bound near the dimer interface, and its binding site encompasses residues from both subunits (Crane et al., 1998; Raman et al., 1998). It has become clear that BH4 is essential for catalysis and its function is more and more elucidated.

All three NOS isoforms appear to be active only in its dimeric form (Alderton et al., 2001). Dimerization created between two oxygenase domains of NOS is one of several posttranslational steps required for conversion into an active enzyme (Siddhanta et al., 1996). NOS dimerization is initiated by heme insertion, which results in rapid conformational changes (Klatt et al., 1996). The heme-containing NOS monomer is an intermediate in dimerization and in the presence of BH₄ and L-arginine, form a stable active dimer (Figure B) (Ghosh et al., 1996).

A critical aspect of NOS function is the requirement for the co-factor BH₄ (Channon, 2004). BH₄ binds close to the heme active site at the interface between the two monomers, interacting with residues from both monomers (Figure B) (Raman et al., 1998). Maintenance and stabilization of NOS dimers is dependent on BH₄, which plays a direct role in the multiple step oxidation of arginine through the N^G-hydroxyl-L-arginine intermediate and the subsequent generation of NO (Channon, 2004).

When BH₄ is limiting or absent, NOS biochemistry is fundamentally altered in a number of ways, not merely by a loss of enzymatic activity. First, NOS dimerization is destabilized, leading to a reduction in the relative proportion of NOS dimers versus monomers present in the cell. Second, NOS catalytic activity becomes uncoupled (Channon, 2004). In this situation, the stoichiometric coupling between the reductase domain and L-arginine oxidation at the active site is lost. However, electron transfer from NADPH through the flavins to molecular oxygen is not inhibited, but results in a formation of O₂[•] and/or H₂O₂ instead of NO (Chalupsky and Cai, 2005; Channon, 2004). BH₄ appears necessary, even not always sufficient to prevent NOS uncoupling.

TETRAHYDROBIOPTERIN SYNTHESIS

BH4 is synthesized de novo from guanosine triphosphate (GTP) by the enzymes GTP-CH 1, 6-pyrovoyl-tetrahydrobiopterin synthase (PTPS), and sepiaterin reductase (SR) (Figure C) (Channon, 2004). BH4 is susceptible to oxidation by reactive oxygen species such as ONOO⁻, forming dihydrobiopterin (BH2) and ultimately biopterin (Channon, 2004). Synthesis of BH4 is also possible through the salvage pathway from the synthetic pterin, sepiaterin, which is metabolized to BH2 by SR and then to BH4 by DHFR (Figure C) (Channon, 2004).

GTP-CH 1 is regulated by transcriptional induction in response to stimuli such as cytokines (Hattori et al., 1997). However, inflammatory stimuli do not appear to greatly up-regulate vascular GTP-CH 1 expression in vivo (Alp et al., 2003). Posttranslational modification of GTP-CH 1 activity by phosphorylation and by feedback inhibition through protein-protein interactions may be important additional regulators of BH4 synthesis (Thony et al., 2000). Furthermore, GTP-CH 1 feedback regulatory protein expression in endothelium is reduced in response to cytokines, resulting in increased BH4 synthesis independent of GTP-CH 1 expression (Werner et al., 2002).

For salvage pathway, there is a limited evidence for DHFR in an in vivo study. It seems to be that BH2 is the preferential form in the cells since BH4 once taken up from the extracellular fluid was immediately oxidized to BH2 (Yamamoto et al., 1997). Moreover, BH4 administered to individual animals was also oxidized to BH2 (Hasegawa et al., 2005). The animals supplemented with BH4 could not increase tissue BH4 level when treated by an inhibitor of DHFR (Sawabe et al. 2004). This implies that DHFR plays a critical role in generation of BH4 via the salvage pathway.

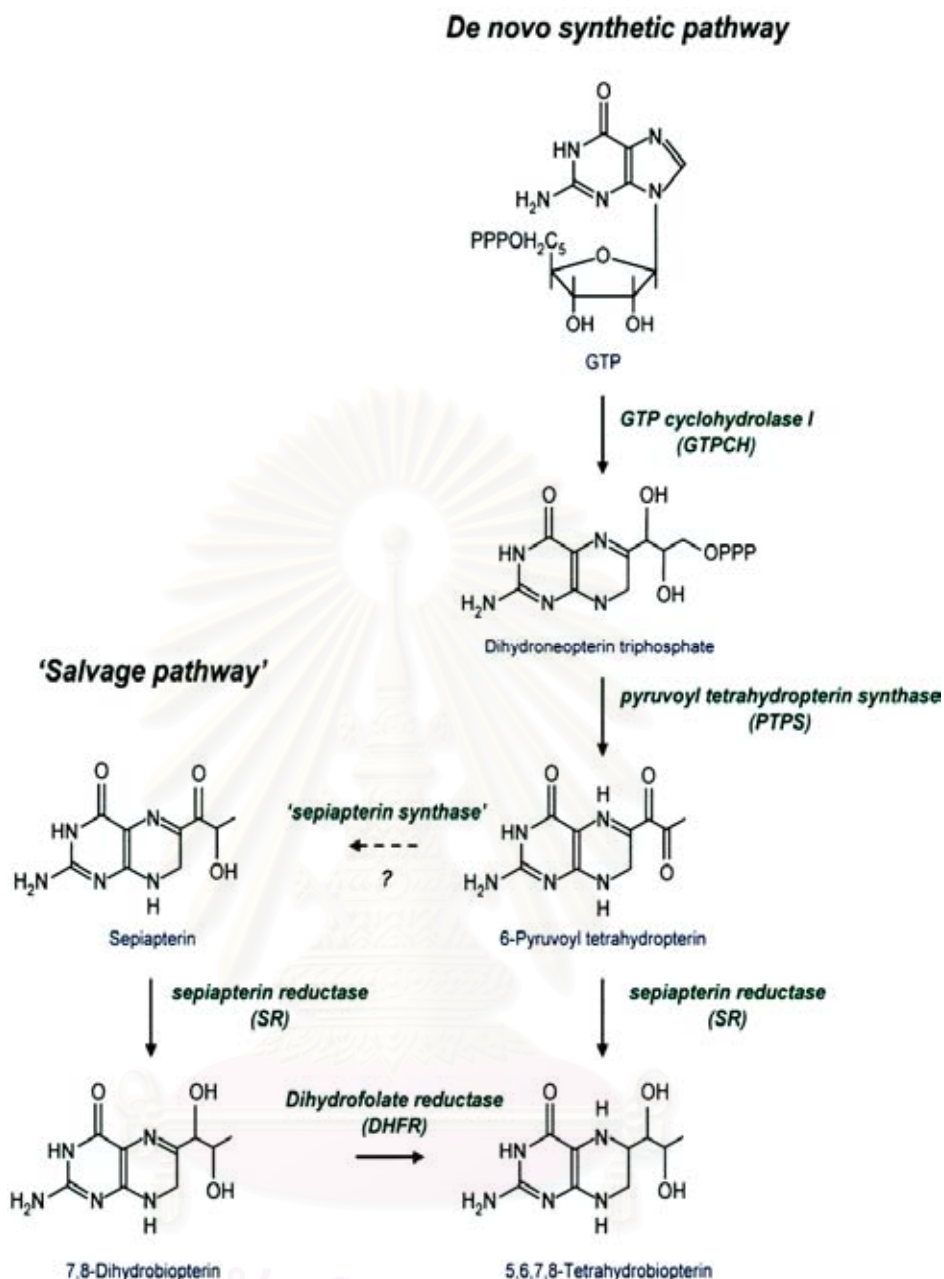


Figure C: Tetrahydrobiopterin (BH₄) biosynthesis and metabolism.

More recent studies have demonstrated the implication of ANG II on DHFR. For instance, ANG II administration (300 ng/kg/min, subcutaneously, osmotic pump) could activate iNOS, NO, O₂^{•-}, and ONOO⁻ generation which are reversed by BH₄ administration (Kase et al., 2005). The similar results also occur in renal IR condition that ANG II is induced. Kakoki et al. (2000) have demonstrated that BH₄

supplementation in IR rats reduces NOS uncoupling as well as increases NO generation and eNOS dimerization. Furthermore, the unveiled action of ANG II on DHFR has been elucidated by Chalupsky and Cai (2005). They have demonstrated that ANG II rapidly and transiently activates NADPH oxidase to produce $O_2^{\cdot -}$, leading to H_2O_2 -dependent down-regulation of DHFR in BAEC. In addition, a second-phase $O_2^{\cdot -}$ production from uncoupled NOS has also been observed (Chalupsky and Cai 2005). The overexpression of DHFR could restore NO production and abolish the changes induced by ANG II (Chalupsky and Cai, 2005). These data demonstrate an essential role of DHFR in maintaining BH₄ and NO bioavailability, and ANG II could modify DHFR under these circumstances. However, the exogenous H_2O_2 could up-regulate GTP-CH 1 expression which increases total biopterin, but the endogenous H_2O_2 produced by ANG II does not enhance GTP-CH 1 (Chalupsky and Cai, 2005; Shimizu et al., 2003). These results suggest that DHFR is much more sensitive to lower endogenous H_2O_2 compared to GTP-CH 1, which is regulated by exogenous H_2O_2 .

Since renal IR causes an increase in ANG II level, it could be postulated that ANG II would affect NOS expression by modulating BH₄ synthesis via alteration in DHFR or GTP-CH 1, or both. However, to date, there is no study on IR in relation to renal DHFR, GTP-CH 1, and NOS expression as well as the role of angiotensin and angiotensin receptor type 1 in this condition. To accomplish these aims, ACEI and ARB were used in the present experiment.

CHAPTER III

MATERIALS AND METHODS

EXPERIMENTAL ANIMALS

The study was performed in male Wistar rats weighing 220 to 250 grams obtained from the National Center of Scientific Use of Animals (Mahidol University, Salaya, Nakhonpathom). The rats were housed in a well ventilated room in which the temperature was 23 to 25°C with an automatic lighting schedule, which provided darkness from 8 p.m. to 6 a.m. The animals were given free access to standard laboratory chow and water as follow the experimental protocol. All rats were used once only. At the end of each experiment, the rats will be terminated with an overdose of sodium pentobarbital by intraperitoneal injection and their remains will be eliminated by burning in an incinerator.

CHEMICALS

Chemical agents

Sodium pentobarbital (Nembutal[®]) was purchased from Sanofi, France. Enalapril[®] (20 mg) was obtained from Biolab, Thailand. Losartan[®] (50 mg) was obtained from M&H, USA. TRIzol[®] reagent was purchased from Invitrogen, USA. Deoxynucleotide triphosphates (dNTPs), Ribonuclease inhibitor, Maloney murine leukemia virus (M-MLV) reverse transcriptase, Taq DNA Polymerase, 100 bp DNA ladder marker, and agarose LE analytical grade were purchased from Promega, USA. Protease inhibitor cocktail was purchased from Sigma, USA. Modified Lowey protein

assay kit and SuperSignal[®] West Pico kit were purchased from Pierce, USA. Prestained protein molecular marker, Laemmli sample buffer, ammonium persulfate, 40% acrylamide/Bis, glycine, TEMED, methanol, sucrose, filter paper, nitrocellulose membrane, and CL-XPosure[™] Film 5 x 7 inches were purchased from Pierce, USA.

Antibodies

Monoclonal anti-dihydrofolate reductase, N-terminal, developed in rabbit (DHFR, Catalog No. D1067), mouse monoclonal antibody against NOS II (inducible NOS, Catalog No. N39020-150), and NOS III (endothelial NOS, Catalog No. N30020-150) were purchased from Sigma, USA. GTP-cyclohydrolase 1 monoclonal antibody (Catalog No. H00002643-M01) was purchased from Abnova Corporation, Taiwan. β -Actin mouse monoclonal antibody (Catalog No. A5441, Sigma, USA) was kindly provided by Assistant Professor Sarinee Kalandakanond-Tongsong, DVM, Ph.D, Faculty of Veterinary, Chulalongkorn University. Blotting grade goat anti-rabbit IgG (H+L) (Human IgG Adsorbed) horseradish peroxidase conjugate (Catalog No. 170-6515) and blotting grade goat anti-mouse IgG (H+L) (Human IgG Adsorbed) horseradish peroxidase conjugate (Catalog No. 170-6516) were purchased from Bio-Rad, USA.

EXPERIMENTAL PROCEDURE

The animals were divided into two main groups sham (S) (n = 24) and IR (n = 24). Each group was further divided into three subgroups, which treated with three different kinds of drinking solution as follow:

1. Water (only distilled water)
2. Water + angiotensin converting enzyme inhibitor, ACEI
(Enalapril[®] 5 mg/kg/day)
3. Water + angiotensin type 1 receptor blocker, ARB
(Losartan[®] 10 mg/kg/day)

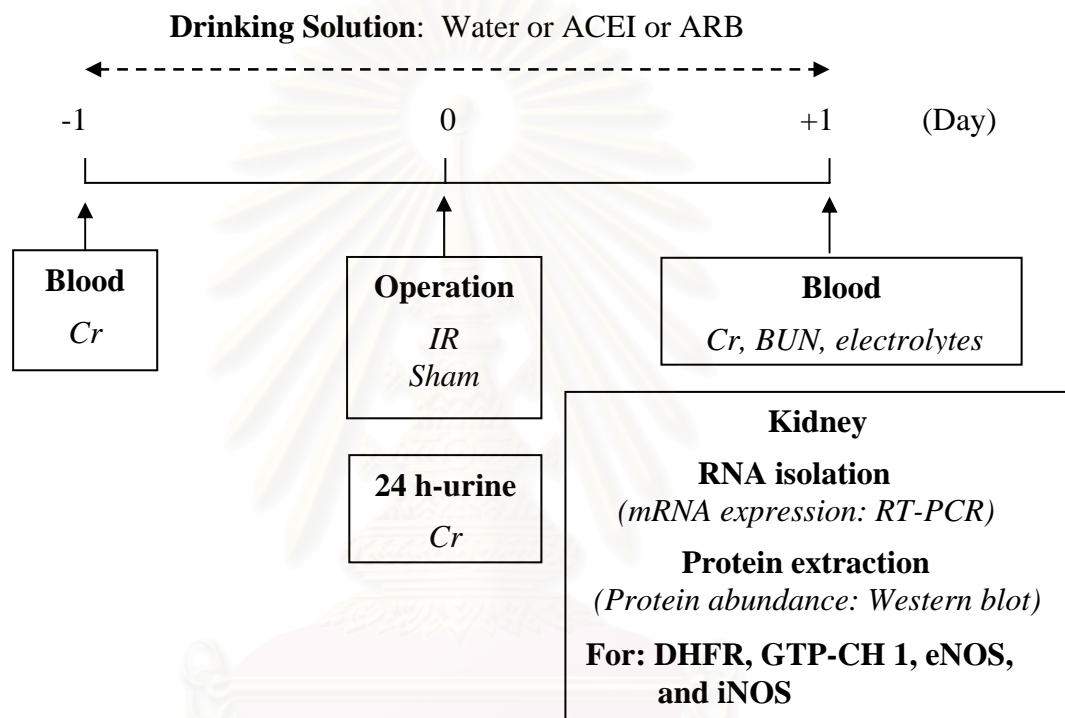
Surgical Operation

After three days of keeping to familiar with the new housing, the rats were weighed and blood samples were collected from the tail for measuring creatinine (Cr) in order to assess kidney function (less than 1 mg %). The rats were anesthetized by intraperitoneal (i.p.) injection of sodium pentobarbital (60 mg/kg body weight). Using aseptic technique, a midabdominal incision was made to expose the kidneys. For IR groups, a unilateral left renal pedicle cross clamp was performed for 30 minutes with microvascular clamps and then was released for reperfusion. The incision was closed. For sham (S) groups, the rats were operated and only wiped left renal pedicle. Each rat was allowed to wake up and return to a metabolic cage with free access to food but with three different kinds of drinking solution as described above.

The volume of drinking solution was approximately 30 ml/rat/day. ACEI or ARB was given one day before the IR or S operation and continuously for 1 day after the operation (n = 8 rats/group). Twenty four-hour urine was collected before the due date. On experimental due date, the rats of respective groups were re-operated. Blood samples were collected from the aorta and centrifuged at 3500 rpm (H-103N, Kokusan, Tokyo, Japan). Serum samples were stored at -80°C until use for blood urea nitrogen (BUN), Cr, and electrolytes measurements by using ISE (ion

selection electrode) indirect method (Model CX3, Beckman, INC, Germany). The kidneys were removed and fixed in liquid nitrogen, and then stored at -80°C until use for RNA isolation and protein extraction.

EXPERIMENTAL DESIGN



DETERMINATION OF mRNA EXPRESSION BY REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION (RT-PCR)

Principal: RT-PCR is a method used to amplify cDNA copies of RNA. With sensitive and versatile, RT-PCR is used to retrieve and clone the 5' and 3' termini of mRNAs and to generate large cDNA libraries from very small amounts of mRNA (Framer and Coen, 2001). In addition, RT-PCR can be easily adapted to identify mutations and polymorphisms in transcribed sequences and to measure the strength of

gene expression when the amounts of available mRNA are limited and/or when the RNA of interest is expressed at very low levels.

The literature is abundantly adorned with descriptions of variants of RT-PCR, many of which have their own acronym. The technical details may vary from one paper to the next, but the underlying concepts are constant and relatively simple. In every case, the first step is the enzymatic conversion of RNA to a single-stranded cDNA template. An oligodeoxynucleotide primer is hybridized to the mRNA and is then extended by an RNA-dependent DNA polymerase to create a cDNA copy that can be amplified by PCR (Framer and Coen, 2001). Depending on the purpose of the experiment, the primer for first-strand cDNA synthesis can be specifically designed to hybridize to a particular target gene or it can bind generally to all mRNAs.

Total RNA Isolation by Using Trizol[®] Reagent

Principal: Total RNA was extracted from the frozen left kidney by using Trizol reagent (Invitrogen, USA). Trizol reagent (cleared-red color) is a ready-to-use reagent for the isolation of total RNA from cells and tissues. The reagent, a mono-phasic solution of phenol and guanidine isothiocyanate, is an improvement to the single-step RNA isolation method developed by Chomczynski and Sacchi (1987). During sample homogenization or lysis, Trizol reagent will disrupt cells and dissolve cell components but the reagent still maintains the integrity of the RNA. The RNA isolation procedure is performed in the sequential steps as follow:

Homogenization

The tissue samples were homogenized in Trizol reagent (1 ml/ 50-100 mg of tissue) by using a polypropylene micropestle (Eppendorf, USA). The sample volume should not exceed 10% of the volume of Trizol reagent used for

homogenization. To remove insoluble material, the homogenate was centrifugated at 12,000xg for 10 minutes at 2 to 8°C (Biofuge Primo R Heracus, Germany). The resulting pellet contains extracellular membranes, polysaccharides, and high molecular weight DNA, while the supernatant contains total RNA. In each sample, the supernatant was transferred to a fresh tube.

Phase separation

To permit the complete dissociation of nucleoprotein complexes, the supernatant samples were added with 0.2 ml of chloroform per 1 ml of Trizol reagent. The tubes were capped securely and shaken vigorously by hand for 15 seconds and incubated them at room temperature (15-30°C) for 2 to 3 minutes. Centrifuge the samples at 12,000xg for 15 minutes at 4°C. Following centrifugation, the mixture separates into a lower red, phenol-chloroform phase, an interphase, and a colorless upper aqueous phase. The RNA remains exclusively in the aqueous phase which is approximately 60% of the volume of Trizol reagent used for homogenization.

RNA precipitation

The aqueous phase was transferred to a fresh tube, and then precipitated by mixing with isopropyl alcohol (0.5 ml/ 1 ml Trizol reagent volume). The samples were allowed to sit for 10 minutes at room temperature and centrifuged at 12,000xg for 10 minutes (4°C). The precipitation of RNA will form a gel-like pellet on the side and bottom of the tube.

RNA wash

The supernatant was removed. The RNA pellet was washed once with 75% ethanol (1 ml/ 1 ml of Trizol reagent used for the initial

homogenization). The pellet was mixed by vortex and then centrifuged at 7,500xg for 5 minutes at 4 °C.

Re-dissolving the RNA

Finally, the RNA pellet was dry briefly (air-dry or vacuum-dry for 5-10 minutes; not by centrifugation under vacuum). It is important not to let the RNA pellet dry completely as this will greatly decrease its solubility. To dissolve RNA, RNase-free water was added into the tube and mixed by passing the solution a few times through a pipette tip. Then, the dissolved RNA solution was incubated for 10 minutes at 55 to 60°C. A portion of dissolved RNA sample was measured the absorbance which should have a ratio of 260/280 at 1.6 to 1.8. The samples were then stored at -80°C until use for cDNA synthesis.

Reverse Transcription (cDNA Synthesis)

To synthesize cDNA, a volume of 1 µg of total RNA was reverse transcribed to a first-strand cDNA in reverse transcription buffer containing 5x reaction buffer, 0.8 mM deoxynucleotide triphosphate (dNTP) mixture, reverse primer of target and house keeping gene glyceraldehyde-3-phosphate-dehydrogenase (GAPDH), 1U/µl Ribonuclease inhibitor, 0.25 U/µl Maloney Murine Leukemia Virus (M-MLV) reverse transcriptase and RNase free water (Promega, USA). The mixture samples were then incubated at 45°C for 45 min and inactivated at 99°C for 5 min by using thermocycler (Perkin Elmer, USA). Then the samples were kept at 4°C until use for amplification.

Polymerase Chain Reaction (cDNA Amplification)

To amplify cDNA, the PCR reaction was performed in a total volume of 50 μ l. A 5 μ l of cDNA was used as templates for subsequent PCR reaction in the thermocycler. The PCR reaction was composed of distilled water, 10x PCR buffer, 2 mM MgCl₂, 200 μ M dNTP mixture, 0.04 U/ μ l Taq DNA polymerase (Promega, USA) and specific oligonucleotide primers (sense and antisense) derived from rat cDNA sequence (www.ncbi.nlm.nih.gov). The primers were designed by using Primer3 Input program (www.cgi v0.2) with base pair length as shown in Table A. The PCR amplification was performed by using PCR thermal programs for 35 cycles under the following condition: denaturation at 94°C for 1 min, annealing for 1 min at different temperatures (Table A) and extension for 90 sec at 72°C. To ensure that equal amounts of cDNA were added to PCR mixture, GAPDH (515 bp) Sense 5'-AATGCATCCTGCACCACCAA-3', and Antisense 5'-GTAGCCATATTCATTGTCATA-3' were also subjected to amplify in the same reaction of each primer pair. In addition, to confirm that there was no genomic DNA contamination in the RNA samples, the PCR reaction was performed without reverse transcription. As a control reaction, the RNase free water was replaced the RNA samples in the reaction.

Table A: Characteristics of the primers that were used for RT-PCR analysis of DHFR, GTP-CH1, eNOS, and iNOS genes in sham and IR rat ^a

Genes Targeted (Accession No.)	Primer Sequences	Product Size (bp)	Annealing Conditions
DHFR (NM_130400)	5'-ACCAGGAAGCCATGAATCAG-3' (S) 5'-AGCAGTAGGACTTGGGAGCA-3' (AS)	224	56°C, 1 min
GTP-CH 1 (NM_024356)	5'-GGGAAGGGTCCATATTGGTT-3' (S) 5'-ACCTCGCATGACCATAACA-3' (AS)	205	55°C, 1 min
eNOS (NM_021838)	5'-TGACCCTCACCGATAACA-3' (S) 5'-CTGGCCTTCTGCTCATTTTC-3' (AS)	210	56°C, 1 min
iNOS (U_03699)	5'-GTGTTCCACCAGGAGATGTTG-3' (S) 5'-GAAGGCGTAGCTGAACAAGG-3' (AS)	272	60°C, 1 min

^a RT-PCR, reverse transcriptase-PCR; DHFR, dihydrofolate reductase; GTP-CH 1, GTP-cyclohydrolase1; eNOS, endothelial NOS; iNOS, inducible NOS; bp, base pair; S, sense primer; AS, antisense primer.

Gel Electrophoresis and Image Analysis

Subsequently, the amplified PCR products were subjected to gel electrophoresis (Bio-Rad, USA), and visualized by High Resolution UV and White Light Gel Doc System (Bio-Rad, USA). Briefly, a 10 μ l of each PCR product was mixed with 2 μ l of loading buffer and then loaded into 1.5% agarose gel containing ethidium bromide. The gel was run at 100 volts (Bio-Rad, USA) until front dye reached the end of gel. Estimated size of PCR products was compared to the standard 100 bp ladder marker (Promega, USA). The intensity of the product bands was quantified by High Resolution UV and White Light Gel Doc System linked to a computer analysis system (Quantity One User Guide for Version 4.2; Bio-Rad, USA). The intensity ratio of each studied gene to GAPDH was calculated.

DETERMINATION OF PROTEIN ABUNDANCE BY USING WESTERN BLOT ANALYSIS

Principal: Immuno-blotting is a widely used and powerful technique for the detection and identification of protein using antibodies. The process involves the separation of sample proteins by polyacrylamide gel electrophoresis (PAGE) followed by transferring of the separated proteins from the gel onto a thin support membrane. The membrane binds and immobilizes the proteins in the same pattern as in the original gel. The membrane (or “blot”) is then exposed to a solution containing antibodies that recognize and bind to the specific protein of interest. The antibodies bound to the membrane are detected by any of a variety of techniques, usually involving treatment with a secondary antibody.

Separation of Protein by

Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE)

Principal: The most widely used method for qualitative analysis of a protein mixture is SDS-PAGE by using the buffer system of Laemmli (1970). With this method, it is possible to determine both the purity and the relative molecular weight of an unknown isolated protein or proteins. In the process, proteins migrate in response to an electrical field through pores in the gel matrix and separate based on molecular size after sample proteins are solubilized by boiling at 100°C, 5 minutes in the presence of anionic detergent and 2-Mercaptoethanol (2-ME). The 2-ME is a disulfide reducing agent, and serves to reduce disulfides holding together the tertiary structure of the protein. The anionic SDS detergent binds strongly to the protein thus disrupting its secondary, tertiary and quaternary structure, resulting in a linear polypeptides chain coated with negatively charged SDS molecules. The binding efficiency of the SDS is generally one SDS molecule for every two amino acid residues. Under this condition, the polypeptide chains are unfold and assumed a rod-like structure and have negative charge, resulting in a constant charge to mass ratio. Then proteins move through a polyacrylamide gel matrix toward the anode. The polyacrylamide gel is cast as a separating gel topped by a stacking gel and secured in an electrophoresis apparatus. Separation is determined by size and therefore when compared to standards of known molecular weight, the relative molecular mass can be estimated. Purity is determined by the presence of a band associated with the desired protein and the absence of bands associated with contaminating proteins.

The SDS gel is comprised of a main separating gel and a stacking gel. The proteins, which have been mixed with a loading buffer, containing on ionizable tracking dye bromophenol blue, are loaded into wells formed in the stacking gel. A

current is passed through the gels and the proteins migrate through the stacking gel and are concentrated into a solid band at the separating gel. When the proteins enter into the separating gel, the negatively charged protein-SDS complexes migrate toward the anode. Their migration in the gel relative to each other is the same based on their uniform negative charge. Separation, therefore, occurs as a result of the molecular sieving properties of the gel. The larger the protein, the more its mobility is retarded by the frictional resistance of the gel the smaller the molecule the further its mobility in the gel. The bromophenol blue is completely unretarded in the gel due to its small size relative to proteins and it is thus used to monitor the progress of the electrophoresis. The current is turned off once the tracking dye has migrated to bottom of the gel. The experimental protocol is performed by the sequential steps as follow:

Assembly of apparatus

The reagents used in preparing the gel should be removed from the refrigerator and allowed to warm and degas for one hour prior to the preparation of the gel. Meanwhile, the sandwich plates were set up for casting the gel. A sandwich consists of two rectangular glass plates: the outer is 10.1 cm (width) x 8.3 cm (height) and the inner is 10.1 cm (width) x 7.3 cm (height) separated by spacers of 0.75 mm thickness (Mini-Protein[®] 3 cell, Bio Rad, Canada). In order to prepare a flawless gel, one containing has no air bubble or debris, the glass plates must be perfectly cleaned and dry with absolute ethanol. The casting clamps were used to mount the outer and inner glass plates facing together.

Preparation of slab gel

For separating gel, 10% or 7.5% acrylamide was carefully filled into the space of sandwich plates from bottom to top with no air bubbles. The height of the gel was adjusted by the comb, approximately 1 cm below the bottom edge. The top layer was filled with 1 ml of distilled water. The gel was allowed to polymerize at room temperature for 30 min. After polymerization, the water was drained off and excess liquid was removed with a piece of Whatman 3 MM paper. The selected comb (number of wells, thickness same as spacers) was gently inserted, then 4% acrylamide solution was filled into the space for making the stacking gel. It should be made sure that no air bubbles formed around the teeth the comb, as they will impede the migration and separation of the proteins. The gel was allowed to polymerize for one hour at room temperature.

Preparation of sample

During polymerizing the stacking gel, equal amounts of total protein from each sample were mixed with sample buffer. The mixers were heat for 5 min at 100 °C in a boiling water bath (Thermostatic bath/circulator; Grant W6, UK). To detect NOS dimer form, the heating step was omitted. The amount of total protein used for total NOS was 50 µg, and for DHFR, GTP-CH1, monomer or dimer of NOS was 100 µg.

Electrophoresis

After polymerization is complete, the comb was gently removed. The wells were filled with running buffer (Appendix). The gel was mounted in the electrophoresis apparatus and the upper buffer chamber was filled with running buffer. Remove any air bubbles trapped at the bottom of the wells. This will disrupt

the electrical circuit and an uneven electrophoresis. Each protein sample was loaded into the bottom of each well. The molecular weight markers (Fermentus, USA) were also loaded. Then, the running buffer was poured into the lower chamber. The electrophoresis apparatus was attached to an electric power supply (PowerPac™ HC, Bio-Rad, USA) and turned on at 125 volt. Small bubbles should start to be produced and rise off the electrode wire at the bottom of the lower chamber. If no bubbles appear then there is an electrical circuit problem. The gel was run until the dye front reaches the bottom of gel. To detect dimer form of NOS the temperature of the gel was maintained below 15°C during electrophoresis (low temperature-PAGE, LT-PAGE). The power supply was turned off. Then, the gel from the glass plate was removed and placed into the transfer buffer.

Protein transfer

A nitrocellulose membrane (Trans-Blot®, Bio-Rad, USA) and two sheets of absorbent filter paper were cut into the same size of the gel. The membrane, filter papers, and support pads were soaked in the transfer buffer for 10 min. The transfer cassette was assembled by lying the black side down, then plate a support pad, filter paper, gel, membrane, filter paper, and support pad. Lock and put the complete transfer cassette into the transfer tank containing transfer buffer by facing the membrane side to the positive electrode (anode, red electrode) and transferred for 120 min at 100 volt. After transfer, the membrane was removed from the cassette and immersed into the blocking solution.

Blocking

The membrane was incubated in blocking solution (5% non fat dry milk in PBS-0.1% Tween) for 1 h at room temperature with gentle rotation on a

platform rocker (Orbital Shaker, UK). This process will reduce the background of non-specific binding site with irrelevant protein. After blocking, the membrane was washed for 10 min 2 times by PBS-0.1% Tween washing buffer.

Detection of bound antibody

The dilution of primary antibody was prepared in PBS-0.1% Tween (1:1000 for DHFR, GTP-CH 1, and iNOS; 1: 500 for eNOS and 1:100000 for β -actin). The membrane, in a clean plastic box, was incubated with the respective primary antibody overnight at 4°C on a platform rocker. After incubation, the primary antibody solution was discarded. The membrane was washed with 20 ml of PBS for 10 min 2 times. The secondary antibody was prepared in PBS-0.1% Tween. The goat anti rabbit IgG conjugated HRP antibody at 1:20,000 dilution was used for DHFR. The goat anti mouse IgG conjugated HRP antibody at 1:20,000 dilution was used for GTP-CH 1, iNOS, and β -actin, and at 1: 5,000 dilution for eNOS. The membrane was incubated in the secondary antibody for 1 h at room temperature on a platform rocker. After that, the blotting membrane was washed with PBS-0.1% Tween for 10 min 2 times on a platform rocker.

Protein detection and image analysis

The blotting membrane was placed on a cleaned glass plate. The detection reagent (SuperSignal[®] West Pico kit, Pierce, USA) was prepared by mixing equal parts of the stable peroxide solution and the luminal/enhancer solution, and then overlay the reagent directly on the membrane surface carrying the protein. After incubation for one min. at room temperature, the excess reagent was drained off, and wrapped by a piece of saran wrap. It is necessary to work quickly once the membrane has been exposed to the detection solution. In a dark room, the membrane

was placed, protein side up, in a X-ray film cassette. The lights were turned off and a sheet autoradiography film (CL-XPosure™ Film 5 x 7 inches, Pierce, USA) was carefully placed on the top of the membrane, then the cassette was closed and exposed for a certain period, eg. 1 min (this depends on the amount of target protein on the membrane). The film was developed by X-Ray film processor (Optimax® 2010, Germany) and scanned the intensity by using high resolution scanner (Image class MPC190, Canon H12260, Canada). Each intensity band was quantified by High Resolution UV and White Light Gel Doc System linked to a computer analysis system (Quantity One User Guide for Version 4.2; Bio-Rad, USA). The intensity ratio of each studied protein to β -actin was calculated.

DETERMINATION OF PROTEIN CONCENTRATION BY LOWRY METHOD

Protein Extraction

Each frozen renal tissue was homogenized on ice with a homogenizer (T25 Basic, IKA, Malaysia) in homogenization buffer (20 mM Tris-HCl; pH 7.5, 2mM MgCl₂, 0.2 M sucrose, and 5% v/v protease inhibitor cocktail, Sigma, USA). The homogenates were centrifuged at 12,000 g for 20 min at 4°C. The resulting pellet containing cell nuclei and tissue debris was discarded. The protein concentration of the supernatant was collected and aliquot into a sterile microcentrifuge tube, kept at -80°C until use. All samples will be further assayed for the amount of protein by using a modified Lowry assay kit (Bio-Rad, USA).

Protein Assay

Principal: For many years, Lowry's method was the most widely used and cited procedure for protein quantitation (Lowry et al., 1951). The procedure involves the reaction of protein with cupric sulfate and tartrate in an alkaline solution, resulting in formation of tetradentate copper-protein complexes. When the Folin-Ciocalteu reagent is added, it is effectively reduced in proportion to these chelated copper complexes, producing a water-soluble product whose blue color can be measured at 750 nm. The protocol is performed by the sequential step as follow:

Preparation of serum bovine albumin (BSA) standards

Five standard dilutions in duplicate (0, 50, 100, 200, and 500 $\mu\text{g/ml}$) were prepared by dissolving the stock standard BSA solution (2 mg/ml) as indicated in Table B. Pipette double distilled deionized water 180, 450, 250, 250 and 200 μl into tube No.1-5, respectively. Then pipette BSA stock (2mg/ml) 60 μl into tube No.1 and 50 μl into tube No.2, mixed each tube thoroughly. Then, pipette 250 μl of solution from tube No.2 into tube No.3 and mixed well. Finally, pipette 250 μl of solution from tube No.3 into tube No.4, then mixed each tube thoroughly. There will be sufficient volume of each diluted standard for two replications.

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Table B: Preparation of serum bovine albumin (BSA) standards

Tube Number	BSA ($\mu\text{g/ml}$)	BSA (μl)	DDW (μl)	Total volume (μl)
1	500	60	180	240
2	200	50	450	500
3	100	250	250	500
4	50	250	250	500
5	0	-	200	200

Note: DDW = Double distilled deionized water

Preparation of 1X Folin-Ciocalteu reagent

Prepare 1X (1 N) Folin-Ciocalteu reagent by diluting the supplied 2X (2 N) reagent 1:1 with ultrapure water. Because the diluted reagent is unstable, prepare only as much 1X Folin-Ciocalteu reagent as will be used in one day. Each test replicate requires 50 μl of 1X Folin-Ciocalteu reagent in the test tube protocol.

Procedure to Quantitate Total Protein

1. Pipette 0.1 ml of each standard and unknown sample replicate into an appropriately labeled test tube.
2. At 15-sec intervals, add 0.5 ml of Modified Lowry Reagent to each test tube. Mix well and incubate each tube at room temperature for exactly 10 min.

3. Exactly at the end of each tube's 10-min incubation period, add 50 μ l of prepared 1X Folin-Ciocalteu Reagent, immediately vortex to mix the contents. Maintain the 15-sec interval between tubes established in step 2.
4. Cover and incubate all tubes at room temperature for 30 min.
5. With the spectrophotometer set to 750 nm, zero the instrument by a cuvette filled only with water. Subsequently, measure the absorbance of all the samples.
6. Subtract the average 750 nm absorbance values of the blank standard replicates from the 750 nm absorbance values of all other individual standard and unknown sample replicates.

CALCULATION FOR ASSESSMENT OF RENAL FUNCTION

$$\text{Creatinine clearance (C}_{\text{Cr}}) = \frac{U_{\text{Cr}} \times V}{P_{\text{Cr}}}$$

STATISTICAL ANALYSIS

All data were expressed as mean \pm SD. For comparison among groups of animals, one way analysis of variance (one-way ANOVA) was used and the differences in pairs of means among groups were made by Tukey's test.

If the statistical probability (p-value) was less than 0.05, the differences were considered to be statistically significant.

CHAPTER IV

RESULTS

Effects of ACEI or ARB on renal DHFR and GTP-CH 1 mRNA expression in S or IR

As shown in Figure 1, in S or S treated groups (with ACEI or ARB), the renal DHFR mRNA expression was comparable (S = 100 %, S + ACEI = 104.79 ± 12.02 %, S + ARB = 103.47 ± 15.36 %). IR significantly decreased the expression to be 66.74 ± 14.46 % ($p < 0.01$ as compared with S or S treated groups). Treatment with ACEI or ARB could restore the DHFR mRNA levels to be 93.54 ± 10.04 % ($p < 0.05$) and 101.52 ± 17.21 % ($p < 0.01$), respectively.

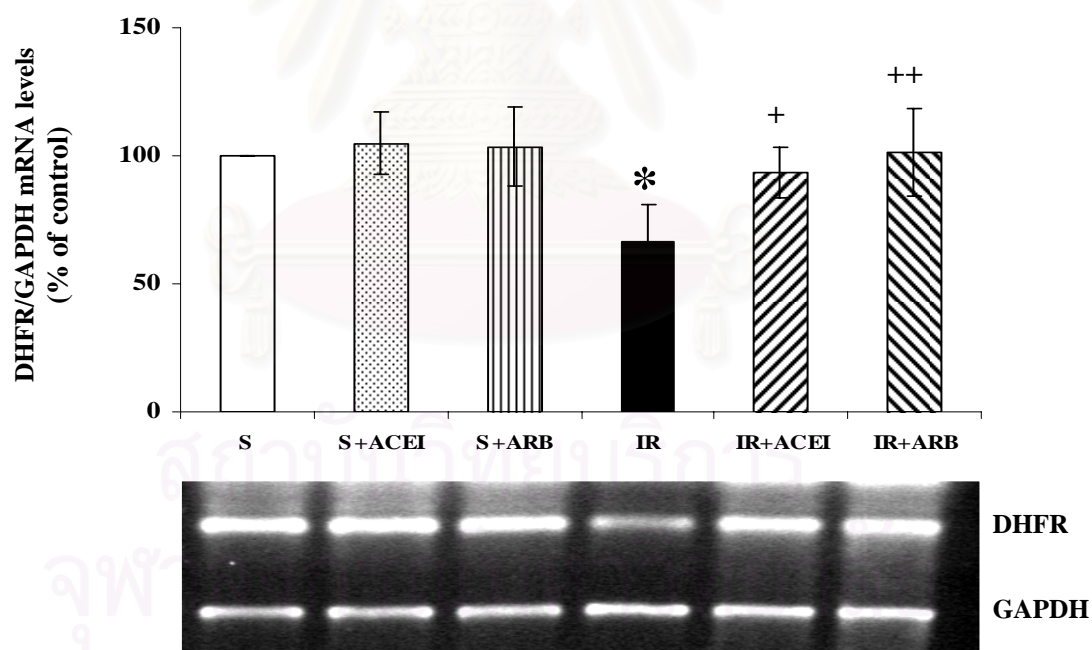


Figure 1: Effects of ACEI or ARB on renal DHFR mRNA expression in S or IR rats (n = 8/group). The upper panel is histogram bars showing the ratio of DHFR to GAPDH intensity. The lower panel is a representative ethidium bromide-stained agarose gel photograph for 515 bp GAPDH mRNA and 224 bp DHFR mRNA. * $p < 0.01$ vs S or S treated groups, + $p < 0.05$, ++ $p < 0.01$ vs IR

For GTP-CH1 (Figure 2), either IR or the inhibition of ANG II had no significant effect on the mRNA levels. The expression was comparable in all groups studied (S = 100 %, S + ACEI = 100.01 ± 9.96 %, S + ARB = 98.33 ± 11.11 %; IR = 101.23 ± 12.81 %, IR + ACEI = 96.54 ± 11.18 %, IR + ARB = 97.54 ± 12.37 %).

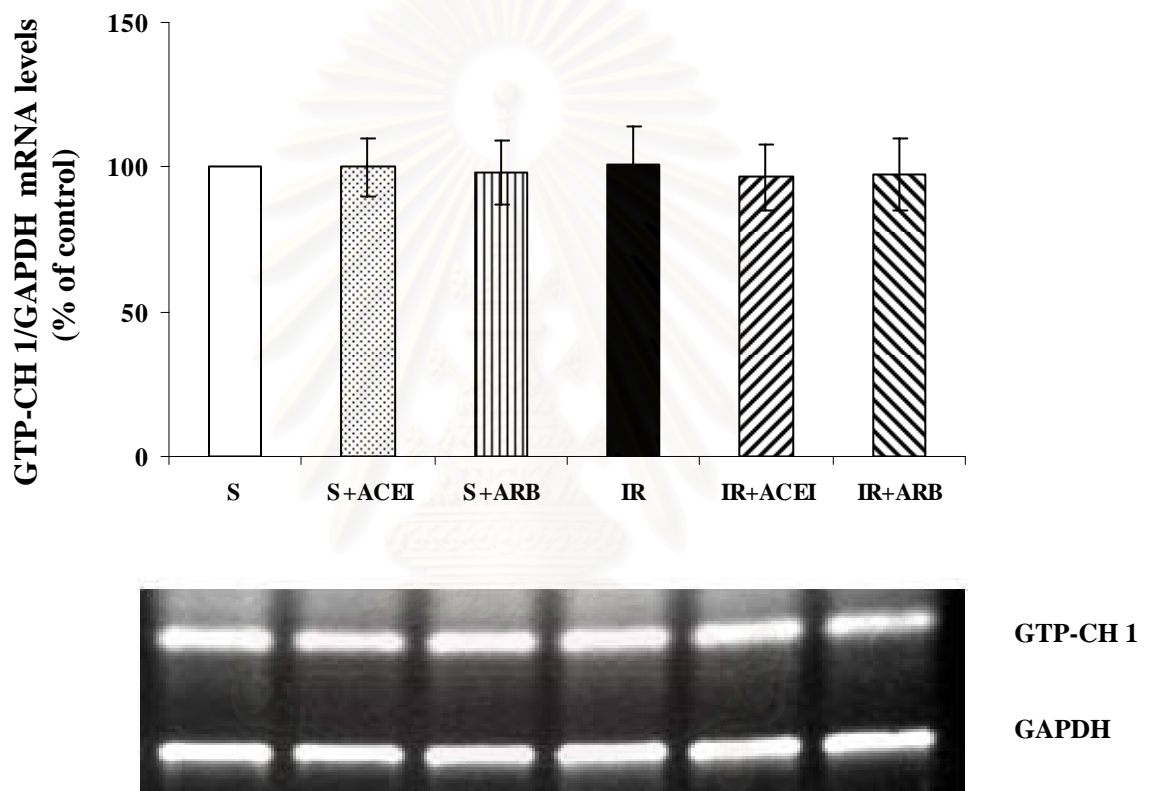


Figure 2: Effects of ACEI or ARB on renal GTP-CH 1 mRNA expression in S or IR rats (n = 8/group). The upper panel is histogram bars showing the ratio of GTP-CH 1 to GAPDH intensity. The lower panel is a representative ethidium bromide-stained agarose gel photograph for 515 bp GAPDH mRNA and 205 bp GTP-CH 1 mRNA.

Effects of ACEI or ARB on renal DHFR and GTP-CH 1 protein abundance in S or IR

As illustrated in Figure 3, IR significantly decreased renal DHFR protein to be $79.57 \pm 7.70 \%$ ($p < 0.01$) as compared with S or S treated groups (S = 100 %, S + ACEI = $102.04 \pm 6.53 \%$, and S + ARB = $105.41 \pm 5.46 \%$). Treatment with ACEI or ARB could restore DHFR protein levels to be $95.31 \pm 6.59 \%$ and $94.95 \pm 6.50 \%$ ($p < 0.01$), respectively.

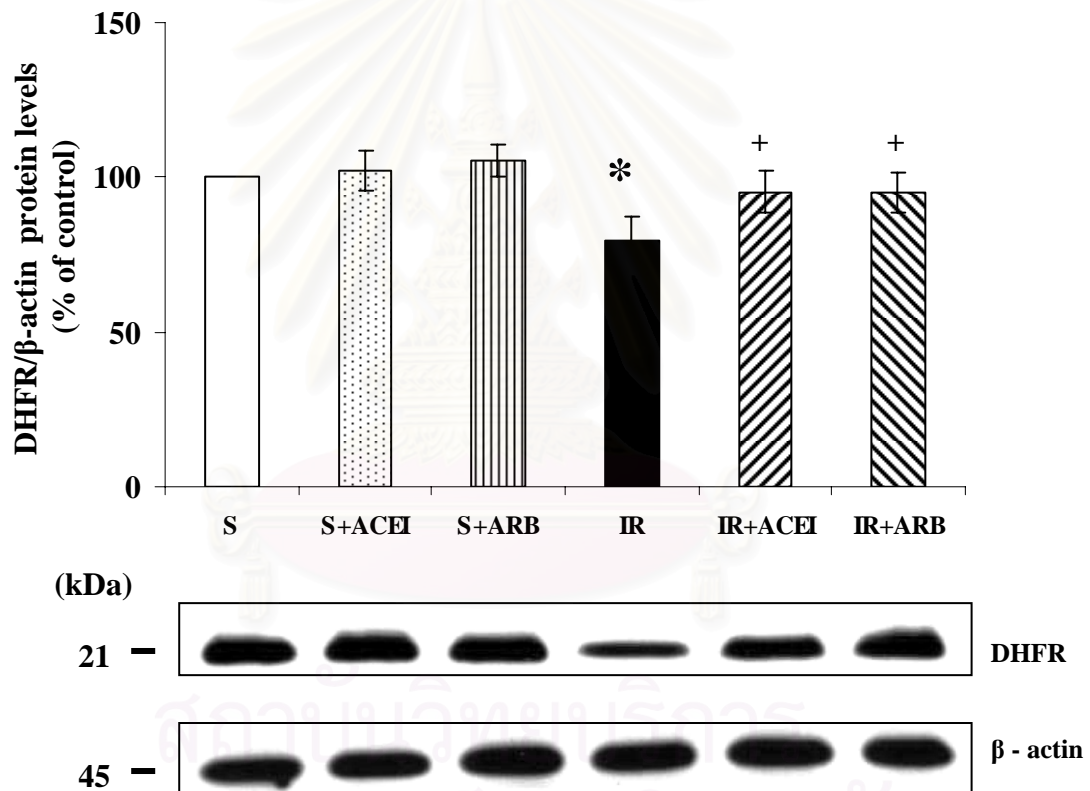


Figure 3: Effects of ACEI or ARB on renal DHFR protein abundance in S or IR rats. The upper panel is histogram bars showing the results of densitometric analyses from pooled data ($n = 8/\text{group}$). Values were normalized by the corresponding optical density for β -actin, used as internal control. The lower panel shows the results of immunoblots analyzed in renal tissue, and probed with antibodies against DHFR (21 kDa) or β -actin (45 kDa). * $p < 0.01$ vs S or S treated groups, + $p < 0.01$ vs IR

For GTP-CH1 (Figure 4), either IR or the inhibition of ANG II had no significant effect on the protein levels. The abundance was comparable in all experimental groups (S = 100 %, S + ACEI = 100.80 ± 9.20 %, S + ARB = 103.98 ± 9.29 %, IR = 106.35 ± 7.35 %, IR + ACEI = 102.45 ± 9.58 %, IR + ARB = 103.06 ± 11.41 %).

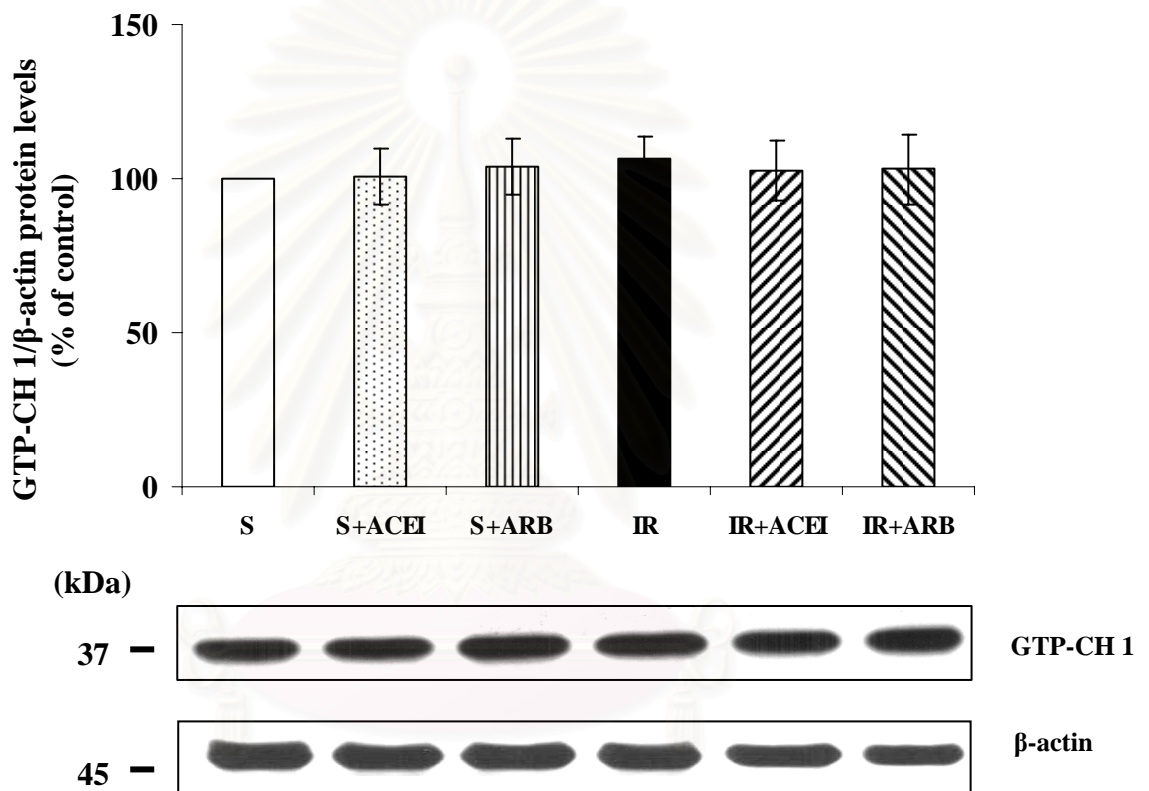


Figure 4: Effects of ACEI or ARB on renal GTP-CH 1 protein abundance in S or IR rats (n = 8/group). The upper panel is histogram bars showing the results of densitometric analyses from pooled data (n = 8/group). Values were normalized by the corresponding optical density for β-actin used as internal control. The lower panel shows the results of immunoblots analyzed in renal tissue, and probed with antibodies against GTP-CH 1 (37 kDa) or β-actin (45 kDa).

Effects of ACEI or ARB on renal eNOS and iNOS mRNA expression in S or IR

For renal eNOS mRNA expression (Figure 5), IR or the inhibition of ANG II did not significantly alter the expression. The mRNA levels were comparable in all groups studied (S = 100 %, S + ACEI = 95.83 ± 18.13 %, S + ARB = 88.13 ± 19.99 %; IR = 94.64 ± 12.38 %, IR + ACEI = 91.46 ± 13.86 %, IR + ARB = 95.21 ± 19.68 %).

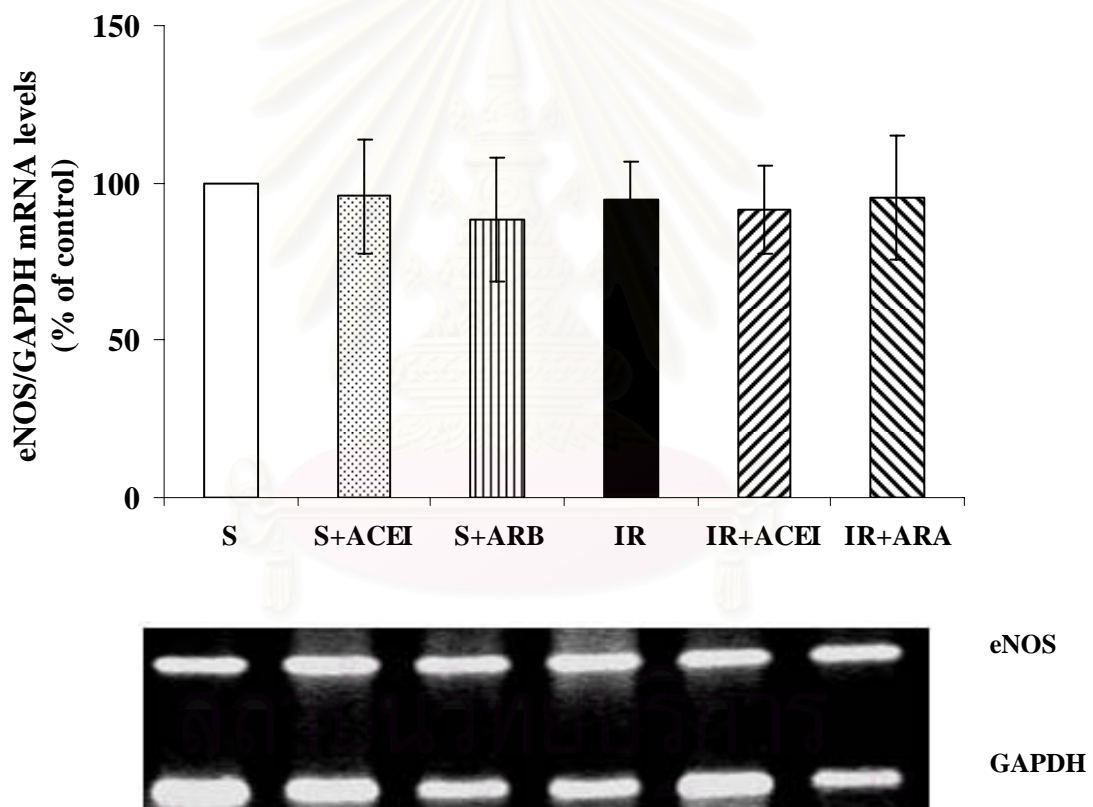


Figure 5: Effects of ACEI or ARB on renal eNOS mRNA expression in S or IR rats (n = 8/group). The upper panel is histogram bars showing the ratio of eNOS to GAPDH intensity. The lower panel is a representative ethidium bromide-stained agarose gel photograph for 515 bp GAPDH mRNA and 210 bp eNOS mRNA.

The renal iNOS mRNA expression (Figure 6) of S rats did not significantly differ from S + ACEI (89.26 ± 20.69 %) or S + ARB (82.33 ± 18.77 %). IR increased the mRNA expression to be 154.35 ± 24.70 % ($p < 0.01$) as compared with S or S treated groups. This heightened level was attenuated by ACEI to be 106.25 ± 17.75 % or by ARB to be 110.87 ± 20.46 % ($p < 0.01$).

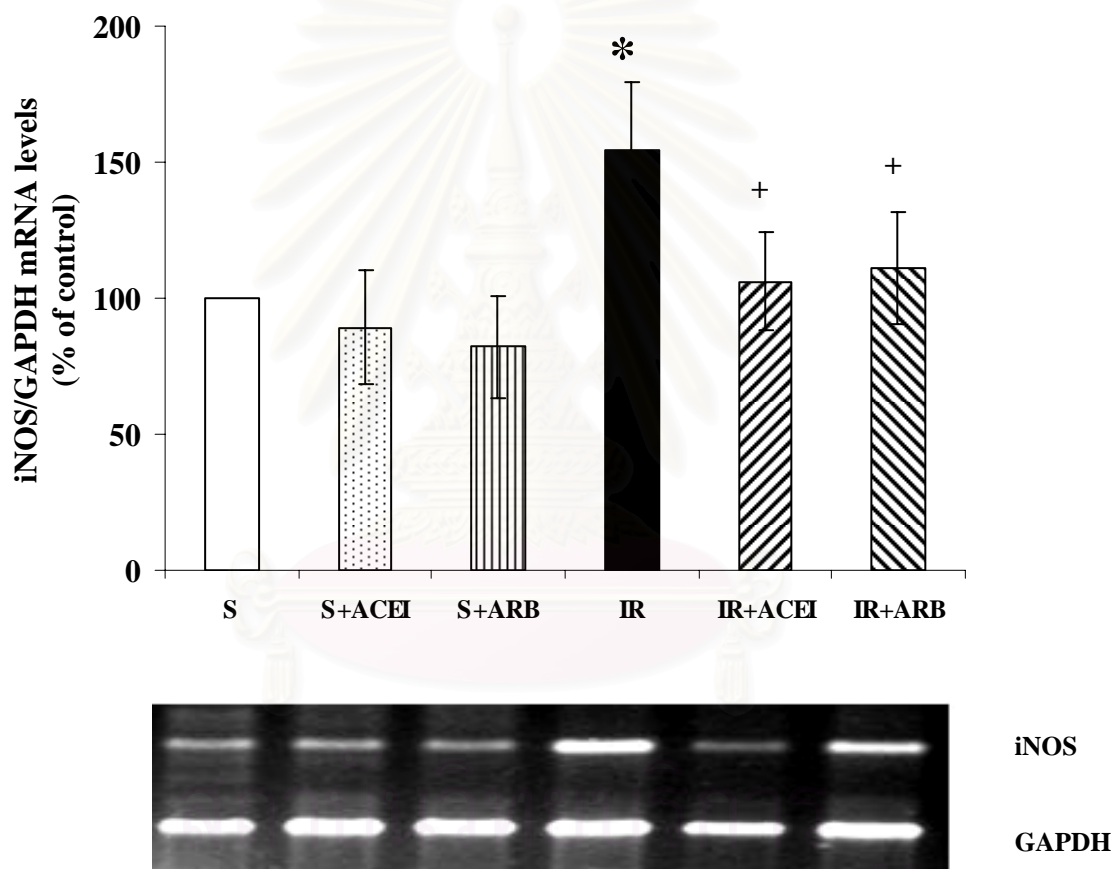
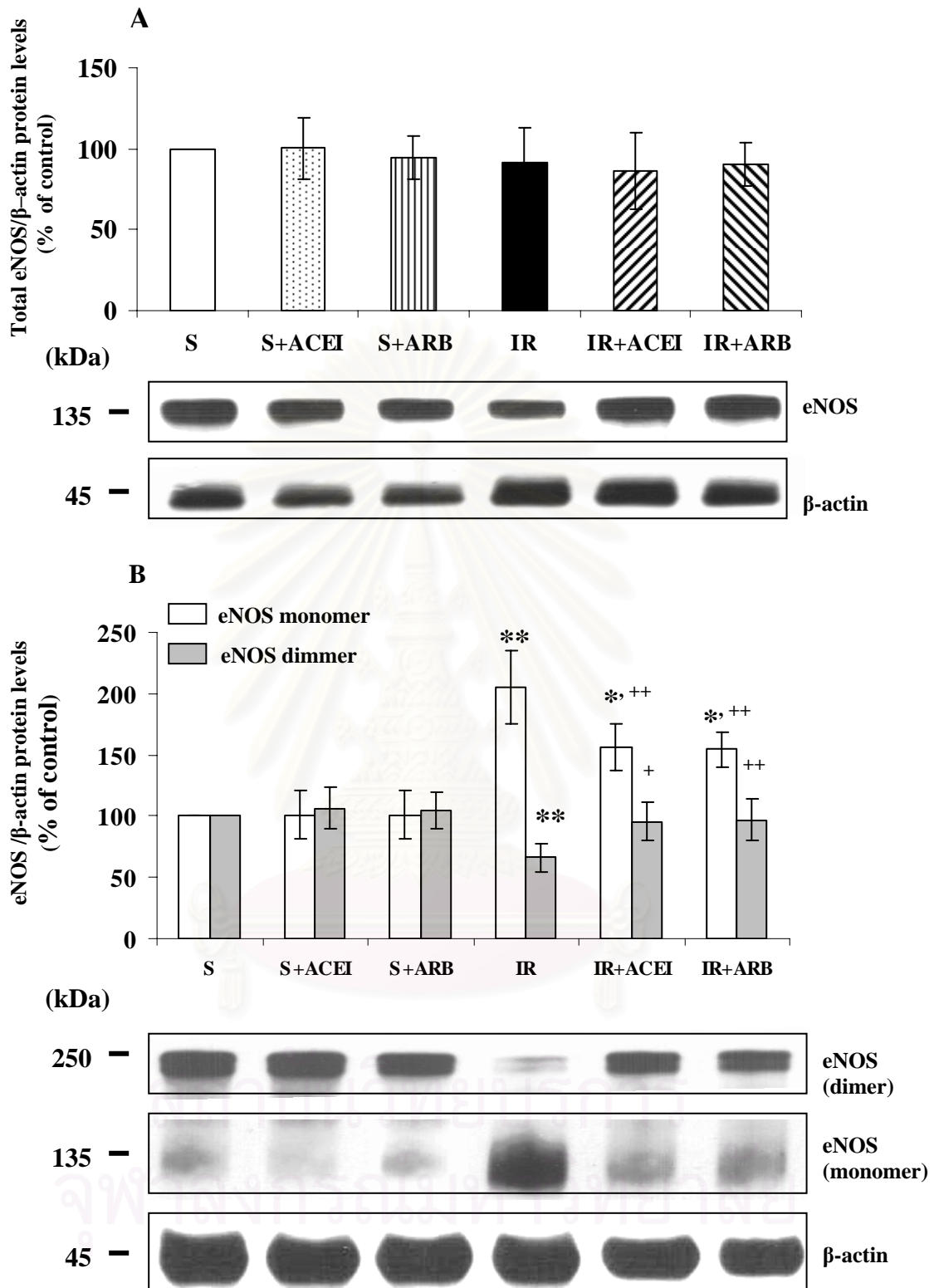


Figure 6: Effects of ACEI or ARB on renal iNOS mRNA expression in S or IR rats ($n = 8/\text{group}$). The upper panel is histogram bars showing the ratio of iNOS to GAPDH intensity. The lower panel is a representative ethidium bromide-stained agarose gel photograph for 515 bp GAPDH mRNA and 272 bp iNOS mRNA. * $p < 0.01$ vs S or S treated groups, + $p < 0.01$ vs IR

Effects of ACEI or ARB on renal eNOS and iNOS protein abundance in S or IR

For total eNOS protein abundance (Figure 7A), the levels did not differ in all experimental groups (S = 100 %, S + ACEI = 100.23 ± 18.61 %, S + ARB = 94.58 ± 13.62 %, IR = 91.52 ± 21.81 %, IR + ACEI = 86.58 ± 23.58 %, and IR + ARB = 90.80 ± 13.36 %). However, after immunoblot analysis (LT-PAGE) (Figure 7B), the data showed that eNOS monomer form (135 kDa) was increased from S or S treated groups (S = 100 %, S + ACEI = 101.01 ± 20.07 %, and S + ARB = 101.08 ± 19.78 %) to be 205.07 ± 29.45 % in IR group ($p < 0.01$). Either ACEI or ARB could attenuate the heightened levels to be 156.42 ± 18.72 % by ACEI or to be 154.39 ± 14.68 % by ARB ($p < 0.01$). However, these levels were still significantly higher than S or S treated rats ($p < 0.05$).

By contrast, the dimer form was significantly decreased from S or S treated groups (S = 100 %, S + ACEI = 106.37 ± 17.32 %, and S + ARB = 104.72 ± 15.39 %) to be 65.90 ± 11.35 % in IR group ($p < 0.01$). ACEI or ARB could restore the dimer form of eNOS protein abundance to be 95.76 ± 19.91 % ($p < 0.05$) and 95.70 ± 16.96 % ($p < 0.01$), respectively.



The total iNOS protein expression (Figure 8A) of S rat did not significantly differ from S \pm ACEI (99.34 ± 13.91 %) or S \pm ARB (96.38 ± 10.23 %). The level significantly increased in IR group to be 193.75 ± 30.10 % ($p < 0.01$) as compared with S or S treated groups. Either ACEI or ARB could attenuate the heightened levels to be 128.29 ± 24.91 % by ACEI or to be 132.56 ± 25.10 % by ARB ($p < 0.01$).

In immunoblot analysis after low temperature SDS-PAGE (LT-PAGE) (Figure 8B), the immunoreactivity of iNOS monomer form (130 kDa) in S, S + ACEI, and S + ARB were 100 %, 87.84 ± 20.58 %, and 88.85 ± 14.11 %, respectively. The level was evaluated in IR group to be 208.79 ± 8.88 % ($p < 0.01$; as compared with S or S treated groups). ACEI or ARB could normalize the heightened level of iNOS monomer form to be 161.82 ± 20.96 % and 160.81 ± 18.16 % ($p < 0.01$), respectively. However, these levels were still significantly higher than S or S treated rats ($p < 0.01$). Interestingly, the iNOS dimer form did not change significantly in all groups studied (S = 100 %, S + ACEI = 96.57 ± 20.32 %, S + ARB = 87.99 ± 17.92 %, IR = 87.50 ± 16.03 %, IR + ACEI = 105.15 ± 18.69 %, and IR + ARB = 113.24 ± 25.47 %).

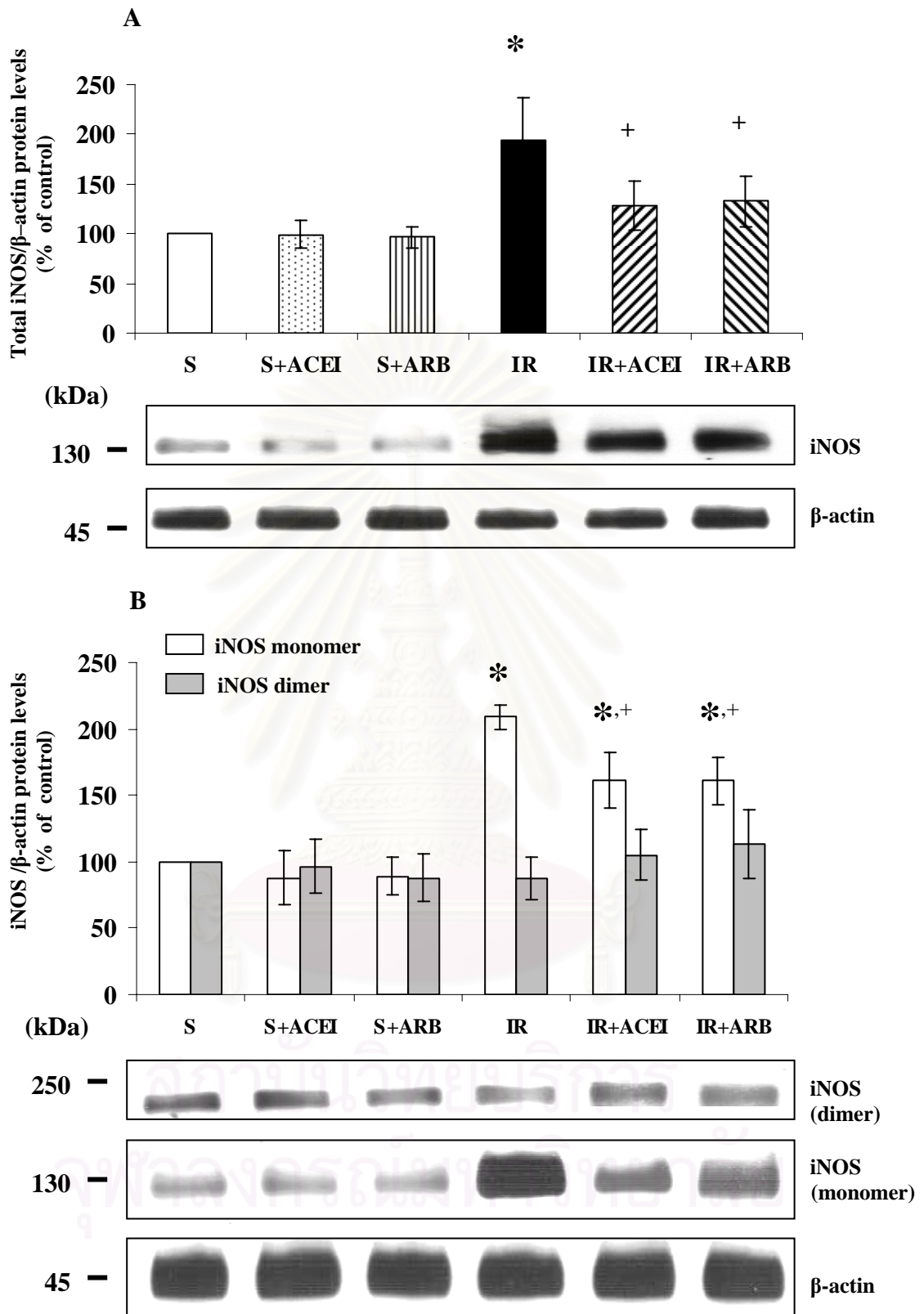


Figure 8: Effects of ACEI or ARB on renal iNOS protein abundant in S or IR rats (n = 8/group). A: representative the results of immunoblots analyzed for total iNOS protein (130 kDa). B: immunoblot after LT-PAGE for iNOS monomer and dimer form. * p<0.01 vs S or S treated groups, + p<0.01 vs IR

Metabolic Parameters in Serum Chemistry and Renal Function

Serum concentrations of Na^+ , K^+ , Cl^- , BUN and Cr in all groups studied showed comparable levels (Table 1). As predicted, creatinine clearance and urine flow rate (Table 1) were not significantly altered by IR or treatment with either ACEI or ARB (Table 1).



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Table 1: Metabolic and renal function profiles of S and IR rats treated with or without ACEI or ARB^b

Parameters	S	S + ACEI	S + ARB	IR	IR + ACEI	IR + ARB
Na ⁺ (mmol/L)	140 ± 1.47	142 ± 1.45	142 ± 1.06	136 ± 1.02	138 ± 1.02	141 ± 1.03
K ⁺ (mmol/L)	3.39 ± 0.23	4.12 ± 0.21	4.01 ± 0.22	4.06 ± 0.17	4.21 ± 0.16	4.13 ± 0.17
Cl ⁻ (mmol/L)	101 ± 1.63	103 ± 1.61	102 ± 1.16	100 ± 1.17	99 ± 1.16	102 ± 1.18
BUN (mg%)	20.16 ± 0.06	24.01 ± 0.98	25.11 ± 1.01	23.39 ± 1.88	25.30 ± 1.99	26.71 ± 1.12
Cr (mg%)	0.44 ± 0.04	0.52 ± 0.05	0.50 ± 0.04	0.52 ± 0.05	0.48 ± 0.04	0.56 ± 0.05
CCr (ml/min/100gBW)	0.72 ± 0.02	0.68 ± 0.03	0.76 ± 0.06	0.60 ± 0.08	0.80 ± 0.05	0.62 ± 0.07
Urine flow rate X10 ⁻² (ml/min)	2.01 ± 0.08	1.99 ± 0.06	2.04 ± 0.05	1.89 ± 0.09	2.03 ± 0.16	2.19 ± 0.09

^bS, Sham; IR, renal ischemic reperfusion; ACEI, angiotensin converting enzyme inhibitor; ARB, angiotensin II receptor type 1 blocker; BUN, blood urea nitrogen; Cr, creatinine; CCr, creatinine clearance; BW, body weight.

CHAPTER V

DISCUSSION AND CONCLUSION

The results in the present study have demonstrated that IR significantly reduced renal DHFR mRNA and protein expression. Either ACEI or ARB could restore the levels to sham groups. This indicates an essential role of ANG II, which was stimulated in renal IR, in reducing DHFR expression. Of interest, this concurs with a recent study in BAEC, which demonstrated that ANG II could impair DHFR expression (Chalupsky and Cai, 2005). ANG II rapidly and transiently activated NADPH oxidase to produce O_2^{\bullet} leading to H_2O_2 -dependent down-regulation of DHFR (Chalupsky and Cai, 2005). In consequence, decreased DHFR levels could induce a deficiency in BH4 which caused NOS uncoupling and production of O_2^{\bullet} instead of NO (Chalupsky and Cai, 2005; Kakoki et al., 2000). Overexpression of DHFR could correct all the above alterations in ANG II-stimulated cells (Chalupsky and Cai, 2005). Moreover, the present study reveals that renal IR with or without ANG II inhibiting agents had no effect on GTP-CH 1 mRNA and protein expression. The results are in agreement with a previous study in non IR model, which showed that endogenous H_2O_2 produced by ANG II did not modulate GTP-CH 1 (Chalupsky and Cai, 2005; Shimizu et al., 2003). Indeed, a recent study illustrated that the exogenous H_2O_2 , the magnitude of which was much higher than the endogenous origin, could up-regulate GTP-CH 1 expression and enhanced BH4 synthesis (Shimizu et al., 2003). Taken together, in IR model, DHFR is much more sensitive to endogenous H_2O_2 when compared with GTP-CH 1.

As mentioned earlier, both GTP-CH 1 and DHFR are important enzymes to produce BH4 in the de novo and salvage pathway, respectively (Alp and Channon,

2004; Thony et al., 2000). In this present work, there was no change of renal GTP-CH 1 but renal DHFR level decreased during IR condition. The results imply that BH4 synthesis may reduce, and then could alter NOS function. Therefore, in this study both iNOS and eNOS expression were measured in the renal tissue simultaneously with DHFR and GTP-CH 1 levels.

For eNOS expression, the present data illustrate that IR or angiotensin inhibition did not alter renal eNOS mRNA and total protein expression. This indicates that IR, in the present study, has no influence on eNOS transcription and translation. However, Kakoki et al. (2000) have demonstrated that total eNOS protein expression significantly increased in rat kidneys subjected to ischemia for 45 min and reperfusion for 1 day. The eNOS mRNA expression was not examined simultaneously, though. Indeed, the expression of eNOS in ischemia condition are under controversy in which it was enhanced (Valdivielso et al., 2001; Vinas et al., 2006; Zheng et al., 2005) or reduced (Kobayashi et al., 2001; Komurai et al., 2003; McQuillan et al., 1994). This discrepancy seems to be associated with the duration of ischemic period or/and the amount of ANG II being available. For example, an acute ANG II infusion (110 minutes) increased eNOS mRNA in kidney by 70% without changing eNOS protein levels, whereas a chronic infusion (10 days) enhanced eNOS protein by 90% without changing eNOS mRNA levels (Hennington et al., 1998). Moreover, Moreno et al. (2002) have also shown that ANG II infusion for 3 h increased renal eNOS activity without modification of their protein expression while a chronic ANG II (3 d) could augment the protein expression but not the activity. Furthermore, the action of ANG II in the kidney is likely to be area specific regulation on NOS expression. For instance, ANG II administration could up-regulate eNOS mRNA and protein in renal cortex, but not in renal medulla (Chin et al., 1999; Navar et al., 2000).

As with no alteration in the total eNOS protein performed by conventional immunoblot analysis, LT-PAGE revealed that the immunoreactivity for dimeric eNOS was significantly decreased whereas the amount of eNOS monomer was enhanced in IR condition. These present data are similar to those evidences studied by Kakoki et al. (2000). They concluded that BH4 was depleted during IR resulting in eNOS monomerization. The dimer form abundance was restored with BH4 supplementation. Therefore, if the BH4 synthesis does not impair during IR, the amount of BH4 would be sufficient and available for dimerization. This would really occur in the present study since the inhibition of ANG II (by ACEI or ARB) could restore DHFR expression which maintains BH4 levels during IR. Thus, the eNOS dimeric form are stabilized. These present results are in the same manner as those performed by Chalupsky and Cai (2005) that ANG II down-regulated DHFR expression and lowered BH4 levels in endothelial cell culture. The inhibition of ANG II action could converse those alterations.

For iNOS, the present data demonstrate that IR activated renal iNOS mRNA expression which is similar to previous studies (Docherty et al., 2006; Vinas et al., 2006). This may explain by the activating effect of various cytokines induced in IR (Araki et al., 2006; Daha et al., 2000; Donnahoo et al., 1999) or by ANG II (Sahar et al. 2005; Ushio-Fukai et al. 1998; Zoja et al., 1998). According to increase iNOS mRNA, the induction of total iNOS protein ensued. ANG II inhibitors, ACEI or ARB, could attenuate these heightened levels. This indicates that both transcription and translation of iNOS were modified during IR, via ANG II through AT1 receptor. In addition, the inhibition of ANG II would suppress activating cytokines and then reduce iNOS mRNA as well as total protein abundance.

By LT-PAGE, the immunoreactivity demonstrated that IR had no effect on iNOS dimer whereas the monomer was markedly enhanced. This indicates that the monomeric form was accounted for the higher level of total protein. Indeed, the iNOS dimer should be formed more as its monomer forms were ready to be dimerized. This, again, may explain by the depletion of BH4 during IR.

Interestingly, in the presence of ANG II inhibition, the amount of BH4 was not depleted which could promote dimerization. However, the dimeric iNOS proteins were constant. The exact mechanisms of this discrepancy remain unclear. One of the most proposed mechanisms for explanation is the inhibitory and regulatory effect of NO, as a heme iron ligand, a cysteine modifying, and an inhibitor of dimerization. It has been found that NO produced from the catalytic reaction in iNOS not only can rebind to the heme iron, thereby directly inhibiting the turnover of the enzyme (Abu-Soud et al., 1995; Abu-Soud et al., 2001), but also it can induce monomerization of the functional dimers (Chen et al., 2002). Binding of L-arginine to the enzyme shifted the monomer to be the loose dimeric state, whereas BH4 will lock the enzyme in a “tight” dimeric state that resisted to NO-induced monomerization (Li et al., 2006). This NO-induced monomerization in the “loose”-dimer was associated with the formation of an intramolecular disulfide bond between C104 and C109, located in the Zn binding motif in the dimer interface (Li et al., 2006). It was shown that the NO-induced monomers can not be reverted back to the dimeric state by the addition of L-arginine and BH4 (Chen et al., 2002). Another type of dimer inhibition of NO in iNOS has been demonstrated in the RAW 264.7 mouse macrophage cell line (Albakri 1996). In that work, they found that endogenous NO produced by iNOS induced by cytokines down-regulated the formation of iNOS into the dimer by preventing heme insertion and decreasing heme availability despite continued accumulation of the

monomer. The dimer inhibition of NO has been reported in eNOS as well. Ravi et al., (2004) discovered that exogenous NO induced S-nitrosylation of Cys thiol groups in the Zn binding motif causing Zn tetrathiolate cluster and sulfhydryl group destruction at the dimer interface, thereby reducing the dimer level and the associated enzymatic activity. S-nitrosylation has also been reported in iNOS by Mitchell et al. (2005). The autoinhibition by NO is hypothesized as a cytoprotective mechanism to suppress NO overproduction (maintain dimer level) and reduce O_2^{\bullet} generation (inactivate monomer form) (Li et al., 2006). Therefore, during angiotensin inhibition, the slightly higher levels of NOS monomer observed in the present study would be likely not much harmful as predicted since the renal tissue damage and lipid peroxidation induced in IR were lessened when treated with ACEI or ARB (Seujange et al., 2006).

The alternative mechanism that has been investigated intensively is protein inhibitors. It was found that, in macrophage cells, a physiological iNOS specific dimerization inhibitor, designated as NAP110 (NOS-associated protein-110 kDa), was upregulated by IFN- γ and LPS in vivo (Ratovitski et al., 1999a). NAP110 binds to iNOS in the amino-terminus region (residues 1-70), a region that is not homologous to the other isoforms, thereby selectively inhibiting its dimerization. Similarly, Kalirin, a large cytosolic protein with nine spectrin-like repeated, inhibited dimerization of iNOS in neuronal cells by binding in the same region (Ratovitski et al., 1999b). In both cases the protein binds to iNOS monomers but does not convert dimers back into the monomeric form. In view of the potential importance of the dimer inhibitory pathway, a number of highly selective synthetic iNOS dimerization inhibitors have been developed, which show great therapeutic potential in iNOS-related pathologies (Blasko et al., 2002; Kolodziejcki et al., 2004). Further studies are needed to elucidate whether these protein inhibitors are also induced in IR condition, or not.

In conclusion, the present study demonstrates the first evidence indicating that IR, via stimulation of ANG II, suppresses renal DHFR but activates iNOS both mRNA and protein expression. IR enhances the monomer while diminishes the dimer form of eNOS. Inhibition of ANG II by using ACEI or ARB could restore DHFR and eNOS dimer whereas attenuate the heightened levels of iNOS expression and NOS monomer. IR has no effect on GTP-CH 1 expression. The present result also indicates that angiotensin II receptor type 1 plays a crucial role in modulation of DHFR and NOS expression.



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สถาบันวิทยบริการ
จุฬาลงกรณ์มหาวิทยาลัย



APPENDIX

สถาบันวิทยบริการ
จุฬาลงกรณ์มหาวิทยาลัย

RT-PCR AND WESTERN BLOT SPECIFIC BUFFER

Buffers preparations for RT-PCR

10x Ficoll loading buffer 10 ml

Fillcoll	25.00	g
Bromphenol blue	0.025	g
0.5 M EDTA (pH 8.0)	0.20	g

Adjust volume to 10 ml with dH₂O, Store at -20 °C

1.5% Agarose gel (w/v) 100 ml

Agarose	1.50	g
1x TBE	100.00	ml

Dissolve by heating and occasional mixing until no granules are visible.

Add ethidium bromide (stock 10 mg/ml) 10 µl (final concentration 1 µg/ml)

10x TBE buffer (pH 8.0) 1 liter

Tris base	54.00	g
EDTA 2H ₂ O (pH 8.0)	20.00	ml
Slowly add the boric acid, anhydrous	27.50	ml

Adjust the pH to 8.0 with conc. HCl

Adjust the volume to 1 liter with dH₂O

1x TBE buffer 1 liter

10x TBE buffer	100.00	ml
dH ₂ O	900.00	ml

Adjust the pH to 7.4 with conc. HCl

Adjust the volume to 1 liter with dH₂O

Preparation of the solutions for tris/glycine SDS-polyacrylamide gel electrophoresis for Western blot

Reagents	10% Separating gel (ml)	7.5% Separating gel (ml)	4% Stacking gel (ml)
H ₂ O	4.67	5.295	3.08
40% acrylamide mix	2.50	1.875	0.50
1.5 M Tris (pH 8.8)	2.50	2.50	1.25
100% Glycerol	0.24	0.24	0.12
20% SDS	0.05	0.05	0.025
10% APS	0.03	0.03	0.01875
TEMED	0.01	0.01	0.00625
Total volume	10.00	10.00	5.00

Buffers preparations for Western blot

1.5 M Tris base (pH8.8) 100 ml

Tris base 18.171 g

dH₂O 80.00 ml

Adjust the pH to 8.8 with conc. HCl and conc. NaOH

Adjust the volume to 100 ml with dH₂O

1 M Tris base (pH6.8) 100 ml

Tris base 12.14 g

dH₂O 80.00 ml

Adjust the pH to 6.8 with conc. HCl and conc. NaOH

Adjust the volume to 100 ml with dH₂O

0.5 M Tris-HCl 100 ml

Tris base	6.00	g
dH ₂ O	40.00	ml

Adjust the pH to 6.8 with conc. HCl and conc.

Adjust the volume to 100 ml with dH₂O

10% SDS 100 ml

SDS	10.00	g
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Adjust the volume to 100 ml with dH₂O

1x Triton lysis buffer 100 ml

25 mM Tris-HCl (pH 8.0)	0.40	g
150 mM NaCl	0.88	g
0.5% Triton X-100	0.50	ml
5 mM EDTA	0.186	g
dH ₂ O	100.00	ml

10x Laemmli running buffer (pH 8.3) 1 liter

Tris base	30.30	g
Glycine	144.20	g
SDS	10.00	g
dH ₂ O	900.00	ml

Adjust the pH to 8.3 with conc. HCl and conc. NaOH

Adjust the volume to 1 liter with dH₂O

1x Transfer buffer 1 liter

Tris base	5.80	g
Glycine	2.90	g
SDS	0.37	g
Adjust the volume to 800 ml with dH ₂ O		
100% Methanol	200.00	ml

10x TBS washing buffer (pH 7.4) 1 liter

Tris base	30.00	g
NaCl	80.00	g
KCl	2.00	g
dH ₂ O	800.00	ml

Adjust the pH to 7.4 with conc. HCl

Adjust the volume to 1 liter with dH₂O

Blocking buffer

5% non fat dry milk in 0.1% TBS (w/v)

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